



# **STIC Search Report**

## **Biotech-Chem Library**

**To: Fozia Hamud**  
**Location: rem/4d64/4c70**  
**Art Unit: 1647**  
**Wednesday, July 07, 2004**

**From: Beverly Shears**  
**Location: Remsen Bldg.**  
**RM 1A54**  
**Phone: 571-272-2528**

**beverly.shears@uspto.gov**

### **Search Notes**

**Case Serial Numbers 10/076260 and 10/030226 attached.**

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: June 30, 2004, 17:14:53 ; Search time 80 seconds  
(without alignments)  
1222.018 Million cell updates/sec

Title: US-10-076-260-2

Perfect score: 1853

Sequence: 1 MYNGSCRIEIGTISQVMP.....ANSFQSQDQWDHIVEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Maximum March 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseq1990s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2000s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	4	AAG80968 Human nGP
2	1853	100.0	346	4	ABB44522 Human GPC
3	1853	100.0	346	4	AUJ06197 Novel hum
4	1853	100.0	346	4	AUJ04373 Human G-P
5	1853	100.0	346	5	AAE16172 Human G-P
6	1853	100.0	346	5	AAU11401 HM74-like
7	1853	100.0	346	5	AAE17077 Human G-P
8	1853	100.0	346	5	ABB08596 Human lip
9	1853	100.0	346	5	ABG93786 Human G-P
10	1853	100.0	346	5	ABP95599 Human GPC
11	1853	100.0	346	5	AAO14788 Human pur
12	1853	100.0	346	5	AAE24354 Human G-P
13	1853	100.0	346	5	ABP81747 Human che
14	1853	100.0	346	6	ABP56751 Human GAV
15	1853	100.0	346	6	AAO26511 Human G-P
16	1853	100.0	346	6	ABP58453 Human res
17	1853	100.0	346	7	ADC46872 Human TA-
18	1853	100.0	346	7	ABW00810 Human GPC
19	1853	100.0	346	7	ADE40282 Human NOV
20	1853	100.0	346	7	ADE40272 Human NOV
21	1853	100.0	346	7	ADE40278 Human NOV
22	1853	100.0	352	7	ADE40286 Human NOV
23	1849	99.8	346	6	ABB82502 Human TGR
24	1846	99.6	346	7	ADE40274 Human NOV
25	1839	99.2	346	4	ABB44523 Human GPC

## ALIGNMENTS

## RESULT 1

AAG80968  
ID AAG80968 standard; protein; 346 AA.

XX AC AAG80968;

DT 28-AUG-2001 (first entry)

DE Human nGPCR11 #2.

XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;  
signal transduction; schizophrenia; thyroid disorder; renal failure;  
rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
cardiovascular disease; proliferative disorder; hormonal disorder;  
neurological disorder; neuronal disorder; Alzheimer's disease; cancer;  
attention deficit-hyperactivity disorder/attention deficit disorder;  
Parkinson's disease; migraine; senile dementia; inflammatory disease;  
rheumatoid arthritis; autoimmune disorder; respiratory ailment;  
neuroprotective.

OS Homo sapiens.

XX WO200136473-A2;

PN 25-MAY-2001.

PF 16-NOV-2000; 2000WO-US031581.

XX 16-NOV-1999; 99US-0165838P.

PR 17-NOV-1999; 99US-0166071P.

PR 19-NOV-1999; 99US-0166678P.

PR 28-DEC-1999; 99US-0173396P.

PR 22-FEB-2000; 2000US-0184129P.

PR 28-FEB-2000; 2000US-0185421P.

PR 28-FEB-2000; 2000US-0185554P.

PR 02-MAR-2000; 2000US-0186530P.

PR 03-MAR-2000; 2000US-0186811P.

PR 09-MAR-2000; 2000US-0188114P.

PR 17-MAR-2000; 2000US-0190310P.

PR 21-MAR-2000; 2000US-0190800P.

PR 20-APR-2000; 2000US-0198568P.

PR 02-MAY-2000; 2000US-0201190P.

PR 08-MAY-2000; 2000US-0203111P.

PR 25-MAY-2000; 2000US-0207094P.

XX (PHAA } PHARMACIA & UPJOHN CO.

PA Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;

PI ABR48195 Human bla

Age40276 Human NOV  
Abp54312 Human G-P  
Ade40280 Human NOV  
Ade40288 Human NOV  
Ade40284 Human NOV  
Aag80934 Human nGP  
Abg93752 Human G-P  
Aac26512 Mouse G-P  
Aac26513 Rat G-Pro  
Ade40290 Human NOV  
Ade40292 Human NOV  
Abg72361 Rabbit or  
Aau77992 Human inf  
Abg72360 Monkey or  
Abg72358 Human orp  
Aaw94654 G-protein  
Aau04379 Human GPC  
Ade86215 Human GPC  
Aay90672 Human mut  
Abr48195 Human bla

PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;  
XX WPI; 2001-389826/41.  
DR N-PSDB; AAH51038.  
XX  
XX New G protein-coupled receptor (GPCR-x) and its encoding polynucleotide  
PT useful for diagnosing and treating e.g. schizophrenia.  
XX  
XX Claim 37; Page 89; 261pp; English.  
XX  
XX The present invention relates to novel G protein-coupled receptors  
CC {GPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,  
CC 31-38, 40, 41, 53-60} and their coding sequences. The present sequence is  
CC one such G protein-coupled receptor. GPCRs are also known as seven  
CC transmembrane receptors and function in signal transduction. The GPCR-x  
CC coding sequences are useful for screening a human to diagnose a disorder  
CC affecting the brain or a genetic predisposition, specifically  
CC schizophrenia. GPCR-x are useful for identifying compounds useful for  
CC treating schizophrenia. Detection of GPCR-x in a sample is useful as a  
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal  
CC failure, rheumatoid arthritis, CNS disorders, infectious such as HIV-1,  
CC metabolic and cardiovascular diseases, proliferative disorders and  
CC hormonal disorders. Modulators of GPCR-x activity have the utility for  
CC treating neurological disorders, including schizophrenia, ADHD/ADD  
CC (attention deficit-hyperactivity disorder/attention deficit disorder),  
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,  
CC migraine and senile dementia. Additional disorders include inflammatory  
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune  
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory  
CC diseases e.g. inflammatory bowel disease  
XX  
XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 4; Length 346;  
Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCRRTEGTISQWMPPLIVAFVLGALGNVLCGFCFHKMTWKSTVYLFNLVA 60  
DB 1 MYNGSCRRTEGTISQWMPPLIVAFVLGALGNVLCGFCFHKMTWKSTVYLFNLVA 60  
QY 61 DFLLMICLPFRDYLYLRHRRHAFGDI PCRVGLFTLANNRAGSIVFLTVAAADRYFKVWHP 120  
DB 61 DFLLMICLPFRDYLYLRHRRHAFGDI PCRVGLFTLANNRAGSIVFLTVAAADRYFKVWHP 120  
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLNHLVCQETAVSCSFIMESANGWHDIM 180  
DB 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLNHLVCQETAVSCSFIMESANGWHDIM 180  
QY 181 FOLEFPMPIGILFCSFKIWSLRRRQQLARQARMKKATRFIMVVAIVITCYLPSVSAR 240  
DB 181 FOLEFPMPIGILFCSFKIWSLRRRQQLARQARMKKATRFIMVVAIVITCYLPSVSAR 240  
QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMDELPLYFFSSPFKFKYKLIKCSLKPK 300  
DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMDELPLYFFSSPFKFKYKLIKCSLKPK 300  
QY 301 QFGHSKTQPEEMPISNLGRSCISVANSPQSDGQWDPHIVEH 346  
DB 301 QFGHSKTQPEEMPISNLGRSCISVANSPQSDGQWDPHIVEH 346

## RESULT 2

ABB44522  
ID ABB44522 standard; protein; 346 AA.

XX  
AC ABB44522;

XX 28-JAN-2002 (first entry)

XX Human GPCR1a polypeptide SEQ ID NO 2.

XX Human; GPCR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;

KW anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity;  
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;  
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;  
KW infection; human immunodeficiency virus; HIV.  
XX  
XX Homo sapiens.  
XX  
XX WO200174904-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US010241.  
XX  
XX 31-MAR-2000; 2000US-0193664P.  
XX 05-APR-2000; 2000US-0194614P.  
XX 06-APR-2000; 2000US-0195063P.  
XX 06-APR-2000; 2000US-0195066P.  
XX 06-APR-2000; 2000US-0195067P.  
XX 06-APR-2000; 2000US-0195068P.  
XX 06-APR-2000; 2000US-0195069P.  
XX 06-APR-2000; 2000US-0195070P.  
XX 06-APR-2000; 2000US-0195510P.  
XX 21-JUL-2000; 2000US-0219855P.  
XX 27-JUL-2000; 2000US-0221284P.  
XX 28-JUL-2000; 2000US-0221325P.  
XX 11-AUG-2000; 2000US-0224588P.  
XX 11-OCT-2000; 2000US-0239613P.  
XX 18-JAN-2001; 2001US-0262508P.  
XX 23-JAN-2001; 2001US-0263433P.  
XX 30-JAN-2001; 2001US-0263604P.  
XX 29-MAR-2001; 2001US-0265161P.  
XX 29-MAR-2001; 2001US-00823172.  
XX  
XX {CURA-} CURAGEN CORP.

XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;  
XX Padigaru M, Mishnu VS, Tchernev VT, Spytek KA, Li L, Baumgartner JC;  
XX Gusev VY;  
XX  
XX WPI; 2001-639351/73.  
XX N-PSDB; ABA81529, ABA81530.

XX New human G-protein coupled receptor X, GPCR-X, polypeptide useful in  
XX treatment or prevention of GPCR-X associated disorders e.g. cardiomyopathy  
XX or arteriosclerosis, and to screen for antagonists and agonists useful  
XX therapeutically.

XX Claim 1; Page 8; 157pp; English.

XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that  
XX encode G-coupled protein-receptor related polypeptides (ABB44522-  
XX ABB44543). The isolated polypeptide having a sequence differing by no  
XX more than 15 % of amino acid residues from one of 22 amino acid sequences  
XX (for mature forms of the sequences), fully defined in the specification  
XX and corresponding to human G-protein coupled receptor X (GPCR-X)  
XX polypeptides. The polypeptides have potential cardiant.  
XX antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The  
XX polypeptides can be administered therapeutically, especially using gene  
XX therapy and expressing the encoding DNA in vivo, to treat or prevent  
XX GPCR-X-associated disorders, especially in humans. For example, they can  
XX be used to treat/prevent cardiomyopathy, arteriosclerosis, disorders  
XX related to signal processing and metabolic pathway modulation (e.g.  
XX obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple  
XX sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's  
XX disease, Parkinson's disorder, Huntington's disease), immune disorders,  
XX haematopoietic disorders, developmental diseases, neurological disorders,  
XX bacterial, fungal, protozoal and viral infections (e.g. with human  
XX immunodeficiency virus (HIV-1 or HIV-2)). They can be used diagnostically  
XX to determine the presence of or predisposition to a disease associated  
XX with altered levels of the polypeptide in mammals (especially humans) by  
XX detecting alterations in polypeptide expression levels relative to  
XX control samples. They are useful to identify agents binding polypeptide  
XX (e.g. cellular receptors or downstream effectors) and/or agents

61	Db	DFLM C I P E T C Y L R R R R A F G D I P C R V G L T L A M R R A G S I V E L T V A A R Y P K V H P	120
	Qy	H H A V N T I S T R V A A G T C T I W A L V I G T Y L L E N H L C V Q E T A V S C E S P T I M E S A N G H W H D M	180
	Db	H H A V N T I S T R V A A G T C T I W A L V I G T Y L L E N H L C V Q E T A V S C E S P T I M E S A N G H W H D M	180
	Qy	F O L E F F E F P L G I I L F C S E K I V S L R R R Q O L A R Q A R M K K A T F I W A I V E I T C Y L P S V S R	240
	Db	F O L E F F E F P L G I I L F C S E K I V S L R R R Q O L A R Q A R M K K A T F I W A I V E I T C Y L P S V S R	240
	Qy	L Y F L W T V P S S A C D P S V G A L H I T L S P T W N S M L D P L V Y Y F S S P K P K P N K L K I C S L K P	300
	Db	L Y F L W T V P S S A C D P S V G A L H I T L S P T W N S M L D P L V Y Y F S S P K P K P N K L K I C S L K P	300
301	Qy	Q P G H S K T O R P R E M P I N S L G R S C I S V A N S F Q S Q D Q W D P H V E W H	346
	Db	Q P G H S K T O R P R E M P I N S L G R S C I S V A N S F Q S Q D Q W D P H V E W H	346

Search completed: June 30, 2004, 17:21:53  
Job time : 84 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

RUN on: July 3, 2004, 03:46:36 ; Search time 516 seconds  
(without alignments)  
8545.794 Million cell updates/sec

Title: US-10-076-260-1

Perfect score: 1038

Sequence: 1 agtacaacgggctgctg.....ccacattgtgagtgccac 1038

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001as.\*
- 5: Geneseq2001bs.\*
- 6: Geneseq2002s.\*
- 7: Geneseq2003as.\*
- 8: Geneseq2003bs.\*
- 9: Geneseq2003cs.\*
- 10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1038	100.0	1038	6	ABA99236	ABA99236 Human G p
2	1038	100.0	1038	7	AAL53846	AAL53846 DNA of hu
3	1038	100.0	1041	4	AAL51008	AAL51008 Human NGP
4	1038	100.0	1041	5	AAS12581	AAS12581 cDNA enco
5	1038	100.0	1041	5	AAS07946	AAS07946 Human GPC
6	1038	100.0	1041	6	AAD27437	AAD27437 Human G-p
7	1038	100.0	1041	6	ABZ42873	ABZ42873 Human GPC
8	1038	100.0	1041	6	ABZ42873	ABZ42873 Human GPC
9	1038	100.0	1041	6	AAL42499	AAL42499 Human pur
10	1038	100.0	1041	7	ABZ22648	ABZ22648 Human GAV
11	1038	100.0	1041	7	ABZ22648	ABZ22648 Human GAV
12	1038	100.0	1041	9	AAD61654	AAD61654 Human res
13	1038	100.0	1050	4	ABA81530	ABA81530 Human GPC
14	1038	100.0	1050	4	ABA81529	ABA81529 Human GPC
15	1038	100.0	1050	9	ADE40271	ADE40271 Human NOV
16	1038	100.0	1057	9	ADE40285	ADE40285 Human NOV
17	1038	100.0	1057	9	ADE40277	ADE40277 Human NOV
18	1038	100.0	1060	9	ADE40281	ADE40281 Human NOV
19	1038	100.0	1083	6	AAD26371	AAD26371 Human G-p
20	1038	100.0	1372	7	ABZ42592	ABZ42592 Human che
21	1038	100.0	1730	6	AAS18501	AAS18501 cDNA enco
22	1038	100.0	2331	5	AAS12582	AAS12582 Gene enco
23	1038	100.0	2345	5	ADC46871	ADC46871 Human TA-

24	1038	100.0	3612	9	ADC46870	ADC46870 Human TA-
25	1036.4	99.8	1104	9	ADE40273	ADE40273 Human NOV
26	1036.4	99.8	1104	6	AAD39181	AAD39181 Human G p
27	1034.8	99.7	1041	7	ABV73367	ABV73367 Human TGR
28	1034.8	99.7	1104	4	ABA81531	ABA81531 Human GPC
29	1034.8	99.7	1104	9	ADE40275	ADE40275 Human NOV
30	1014	97.7	2580	6	ABQ83131	ABQ83131 Human G p
31	942.4	90.8	961	9	ADE40283	ADE40283 Human NOV
32	942	90.8	961	9	ADE40287	ADE40287 Human NOV
33	942	90.8	961	9	ADE40279	ADE40279 Human NOV
34	888	85.5	888	4	AAH50974	AAH50974 Human NGP
35	888	85.5	888	6	ABS70207	ABS70207 DNA enco
36	724.4	69.8	1668	7	AAL53848	AAL53848 DNA of ra
37	723.4	69.7	742	9	ADE40289	ADE40289 Human NOV
38	722.8	69.6	3251	7	AAL53847	AAL53847 DNA of mc
39	627.4	60.4	646	9	ADE40291	ADE40291 Human NOV
40	627.4	60.4	646	9	ADE40297	ADE40297 Human NOV
41	402.8	38.8	1254	7	ABS57853	ABS57853 Rabbit cD
42	372.4	35.9	1174	6	ABK47759	ABK47759 cDNA enco
43	372.4	35.9	1361	2	AAX16671	AAX16671 G-protein
44	369.2	35.6	1092	5	AAS07952	AAS07952 Human CDN
45	369.2	35.6	1492	9	ADC86214	ADC86214 Human GPC

## ALIGNMENTS

RESULT 1  
ABA99236

ID ABA99236 standard; DNA; 1038 BP.

AC ABA99236;

XX

XX

DT 01-JUL-2002 (first entry)

XX

DE Human G protein-coupled receptor protein TGR13 encoding sequence.

XX Antiinflammatory; anorectic; obesity; inflammation; gene therapy; human;

KW G protein-coupled receptor protein TGR13; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1038

FT /tag= a

FT /product= "G-protein-coupled receptor protein TGR13"

FT /partial

FT /note= "no stop codon"

XX

XX WO200202767-A1.

PN

XX

PD

XX

PF 10-JAN-2002.

XX

XX 02-JUL-2001; 2001WO-JP005711.

XX

PR 04-JUL-2000; 2000JP-00206860.

XX

PR 31-JUL-2000; 2000JP-00235274.

XX

PA (TAKE ) TAKEDA CHEM IND LTD.

XX

XX Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;

XX WPI; 2002-164535/21.

XX P-PSDB; ABB08596.

XX

XX New human lipocyte-originated G protein-coupled receptor proteins TGR13

PT and encoding DNAs, for developing drugs to treat obesity and

XX inflammations, including gene therapy.

XX

PS Claim 6; Page 94-95; 101pp; Japanese.

XX

CC This invention relates to a human lipocyte-originated G protein-coupled

XX receptor proteins TGR13, thought to be antiinflammatory and anorectic in

CC their action. The proteins and encoded DNAs are for use in developing  
 CC drugs to treat obesity and inflammation, including gene therapy. The  
 CC present sequence represents the human lipocyte-originated G protein-  
 CC coupled receptor protein TGR13 encoding sequence  
 XX  
 SQ Sequence 1038 BP; 207 A; 294 C; 277 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 6; Length 1038;  
 Best Local Similarity 100.0%; Pred. No. 5e-287;  
 Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACAAACGGTCTGCTGCGCATCGAGGGGACACCACTCTCCAGGTGATCCGCGG 60  
 DB 1 ATGTACAAACGGTCTGCTGCGCATCGAGGGGACACCACTCTCCAGGTGATCCGCGG 60  
 QY 61 CTGCTCAATGTCGCTTGTGCTGGCGCACTAGGCAATGGGTCGCTGTGGTTTC 120  
 DB 61 CTGCTCAATGTCGCTTGTGCTGGCGCACTAGGCAATGGGTCGCTGTGGTTTC 120  
 QY 121 TGTCTCCACATGAAGACTGGAGCCCGACGACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
 DB 121 TGTCTCCACATGAAGACTGGAGCCCGACGACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
 QY 181 GATTTCTCTTATGATCTGCTGCTTTTTCGACAGACATATTACCTCAGACGTAGACAC 240  
 DB 181 GATTTCTCTTATGATCTGCTGCTTTTTCGACAGACATATTACCTCAGACGTAGACAC 240  
 QY 241 TGGGCTTTTGGGACATCTTCCGAGTGGGCTCTTACGTTGGCCATGACAGGGCC 300  
 DB 241 TGGGCTTTTGGGACATCTTCCGAGTGGGCTCTTACGTTGGCCATGACAGGGCC 300  
 QY 301 GGGAGCATCGTGTTCCTTACGTTGGTGGCTGCGACAGGTATTTCMAAGTGGTCCACCCC 360  
 DB 301 GGGAGCATCGTGTTCCTTACGTTGGTGGCTGCGACAGGTATTTCMAAGTGGTCCACCCC 360  
 QY 361 CACACGGGTGACATATCTCCACGGGTGGCGCTGGCATCGTGTGCTGCACTGTGG 420  
 DB 361 CACACGGGTGACATATCTCCACGGGTGGCGCTGGCATCGTGTGCTGCACTGTGG 420  
 QY 421 GCGCTGTCATCTGGGACAGGTATCTTTGCTGGAGAACCATCTCTGCGTGCAGAG 480  
 DB 421 GCGCTGTCATCTGGGACAGGTATCTTTGCTGGAGAACCATCTCTGCGTGCAGAG 480  
 QY 481 ACGGCGTCTCTGTGAGAGCTTCATGAGTGGCCCAATGCGTGGCATGACATCATG 540  
 DB 481 ACGGCGTCTCTGTGAGAGCTTCATGAGTGGCCCAATGCGTGGCATGACATCATG 540  
 QY 541 TTCCAGCTGGAGTCTTTATGCGCTTGGCATCATCTTATTTGCTCTTCAAGATTGTT 600  
 DB 541 TTCCAGCTGGAGTCTTTATGCGCTTGGCATCATCTTATTTGCTCTTCAAGATTGTT 600  
 QY 601 TGGAGCCTGAGCGGAGCGAGCTGGCCAGACAGGCTCGGATGAAGAGGCGACCCGG 660  
 DB 601 TGGAGCCTGAGCGGAGCGAGCTGGCCAGACAGGCTCGGATGAAGAGGCGACCCGG 660  
 QY 661 TTTCATCATGCTGCTGTCATCATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTA 720  
 DB 661 TTTCATCATGCTGCTGTCATCATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTA 720  
 QY 721 CTCTATTTCTGAGCGTGGCTGGAGTGGCTGGATCCCTCTCTCTCAATGGGCGCTG 780  
 DB 721 CTCTATTTCTGAGCGTGGCTGGAGTGGCTGGATCCCTCTCTCTCAATGGGCGCTG 780  
 QY 781 CACATAACCTCAGCTTTCACCTACATGAACAGCATGCTGATCCCTGCTGCTGCTGCT 840  
 DB 781 CACATAACCTCAGCTTTCACCTACATGAACAGCATGCTGATCCCTGCTGCTGCTGCT 840  
 QY 841 TCAAGCCCTCTTTCCTCCAAAATTTACACAAAGCTCAAAATCTGCACTGTAACCCCAAG 900  
 DB 841 TCAAGCCCTCTTTCCTCCAAAATTTACACAAAGCTCAAAATCTGCACTGTAACCCCAAG 900  
 QY 901 CAGCCAGGACCTCAAAACACAGGCGGAGAGTCCATTTGGAACTCGGTGCG 960  
 DB 901 CAGCCAGGACCTCAAAACACAGGCGGAGAGTCCATTTGGAACTCGGTGCG 960

DB 901 CAGCCAGGACCTCAAAACACAGGCGGAGAGTCCATTTGGAACTCGGTGCG 960  
 QY 961 AGGAGTTGCTATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020  
 DB 961 AGGAGTTGCTATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020  
 QY 1021 CACATTGTTGAGTGGCAC 1038  
 DB 1021 CACATTGTTGAGTGGCAC 1038  
 RESULT 2  
 AAL53846  
 ID AAL53846 standard; DNA; 1038 BP.  
 AC AAL53846;  
 XX  
 DT 13-FEB-2003 (first entry)  
 XX  
 DS DNA of human G-Protein Coupled Receptor gene.  
 XX  
 KW Anorectic; antidiabetic; antilipemic; antiasthmatic; antiinflammatory;  
 KW antiallergic; antianginal; nephrotropic; hepatotropic; immunosuppressive;  
 KW virucide; G-Protein-agonist; G-Protein-antagonist; dyslipidaemia; GPCR;  
 KW G-Protein Coupled Receptor; obesity; diabetes; asthma; bronchitis;  
 KW allergy; angina; glomerulonephritis; hepatitis; allograft rejection;  
 KW human; gene; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1038  
 FT /\*tag= a  
 FT /partial  
 FT /product= "Human GPCR protein"  
 FT /note= "No stop codon"  
 XX  
 PN WO200283736-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 14-FEB-2002; 2002WO-US004397.  
 XX  
 PR 14-FEB-2001; 2001US-0269040P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Elliott SG, Rogers N, Busse LA;  
 XX WPI; 2003-075524/07.  
 XX P-PSDB; AA026511.  
 DR  
 XX New GPCR polypeptide and encoding nucleic acid molecule, useful for  
 PT diagnosis, treatment and/or prevention of diseases associated with GPCR  
 PT polypeptides, such as obesity, diabetes, asthma, allergies, angina and  
 PT hepatitis.  
 XX  
 PS Claim 1; Fig 1; 122pp; English.  
 XX  
 CC The invention relates to a novel isolated G-Protein Coupled Receptor  
 CC (GPCR) protein. The methods and compositions of the present invention are  
 CC useful for diagnosis, treatment, amelioration and/or prevention of  
 CC diseases associated with G-Protein Coupled Receptor (GPCR) polypeptides,  
 CC such as obesity, diabetes, dyslipidaemia, asthma, bronchitis, allergies,  
 CC angina, glomerulonephritis, hepatitis and allograft rejection. This  
 CC polynucleotide sequence represents the DNA encoding the human GPCR  
 CC protein of the invention  
 XX  
 SQ Sequence 1038 BP; 207 A; 294 C; 277 G; 260 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1038; DB 7; Length 1038;  
 Best Local Similarity 100.0%; Pred. No. 5e-287;  
 Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGTACAAAGGTCGTCTCCGCGCATCGAGGGGACACCATCTCCACAGTGATGCCGCGG 60
Db 1 ACGTACAAAGGTCGTCTCCGCGCATCGAGGGGACACCATCTCCACAGTGATGCCGCGG 60
QY 61 CTGCTCATCTGTGCTCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
Db 61 CTGCTCATCTGTGCTCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
QY 121 TGCCTCCACATGAAGACCTGGAAGCCAGCACACTGTTTACCTTTTCAATTTGGCGGTGGCT 180
Db 121 TGCCTCCACATGAAGACCTGGAAGCCAGCACACTGTTTACCTTTTCAATTTGGCGGTGGCT 180
QY 181 GATTTCTCTCTTATGATCTGCCTCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
Db 181 GATTTCTCTCTTATGATCTGCCTCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
QY 241 TGGGCTTTTGGGACATTCCTCGCGAGTGGGCTCTTCAGTTGGCCATGAACAGGGCC 300
Db 241 TGGGCTTTTGGGACATTCCTCGCGAGTGGGCTCTTCAGTTGGCCATGAACAGGGCC 300
QY 301 GGGAGCATCGTGTCTTACGGTGGTGGCTGCGGACAGGTATTTCAAGTGGTCCACCC 360
Db 301 GGGAGCATCGTGTCTTACGGTGGTGGCTGCGGACAGGTATTTCAAGTGGTCCACCC 360
QY 361 CACACGCGGTGAACACTATCTCCACCGCGGTGGCGCTGCGCATCGTCTGCACCTGTGG 420
Db 361 CACACGCGGTGAACACTATCTCCACCGCGGTGGCGCTGCGCATCGTCTGCACCTGTGG 420
QY 421 GCCTCGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACCAATCTCTCGGTGCAAGAG 480
Db 421 GCCTCGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACCAATCTCTCGGTGCAAGAG 480
QY 481 ACGGCGCTCTCCCTGAGAGCTTCATCATCGAGTCGCGCAATGCTGCGCATGATCATCATG 540
Db 481 ACGGCGCTCTCCCTGAGAGCTTCATCATCGAGTCGCGCAATGCTGCGCATGATCATCATG 540
QY 541 TTCACGCTGGAGTTCCTTATGCGCCCTCGGCATCATCTTATTTTCTCTTCAAGATGTT 600
Db 541 TTCACGCTGGAGTTCCTTATGCGCCCTCGGCATCATCTTATTTTCTCTTCAAGATGTT 600
QY 601 TGGAGCTGAGCGGAGGAGAGCTGCGGACAGAGCTCGATGGAAGAGGAGGACCCCG 660
Db 601 TGGAGCTGAGCGGAGGAGAGCTGCGGACAGAGCTCGATGGAAGAGGAGGACCCCG 660
QY 661 TTCATCATGCTGTGTGCAATTTGTGTTTATCATCATGCTTACCTGCGCGAGTGTCTGTAGA 720
Db 661 TTCATCATGCTGTGTGCAATTTGTGTTTATCATCATGCTTACCTGCGCGAGTGTCTGTAGA 720
QY 721 CTCTATTTCTCTGAGCGGTGCGCTCGAGTGCCTGCGATCCCTCTGTCCATGGGCGCTG 780
Db 721 CTCTATTTCTCTGAGCGGTGCGCTCGAGTGCCTGCGATCCCTCTGTCCATGGGCGCTG 780
QY 781 CACATTAACCTCTAGCTTACCTACATGAACAGATGCTGGATCCCTCGGTGTATTTT 840
Db 781 CACATTAACCTCTAGCTTACCTACATGAACAGATGCTGGATCCCTCGGTGTATTTT 840
QY 841 TGAAGCCCTCTCTTCCCAATTTCTACAAAGCTCAAAATCTGCAGTCTGAACCCAG 900
Db 841 TGAAGCCCTCTCTTCCCAATTTCTACAAAGCTCAAAATCTGCAGTCTGAACCCAG 900
QY 901 CAGCCAGGACACTCAAAAACAAAGGCGGAGAGATGCCAATTTTGCAGACCTCGGTGCG 960
Db 901 CAGCCAGGACACTCAAAAACAAAGGCGGAGAGATGCCAATTTTGCAGACCTCGGTGCG 960
QY 961 AGAGTTGTCATAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATCCC 1020
Db 961 AGAGTTGTCATAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATCCC 1020
QY 1021 CACATTTGTCAGTGGCAC 1038
Db 1021 CACATTTGTCAGTGGCAC 1038
```

```
RESULT 3
AAH51008
ID AAH51008 standard; DNA; 1041 BP.
XX
AC AAH51008;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human nPCR11 coding sequence #2.
XX
KW G protein-coupled receptor; nPCR; seven transmembrane receptor;
signal transduction; schizophrenia; thyroid disorder; renal failure;
rheumatoid arthritis; CNS disorder; infection; metabolic disease;
cardiovascular disease; proliferative disorder; hormonal disease;
neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
attention deficit-hyperactivity disorder; attention deficit disorder;
Parkinson's disease; migraine; senile dementia; inflammatory disease;
rheumatoid arthritis; autoimmune disorder; respiratory ailment;
neuroprotective; ds.
XX
OS Homo sapiens.
XX
PN WO200136473-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US031581.
XX
PR 16-NOV-1999; 99US-0165838P.
PR 17-NOV-1999; 99US-0166071P.
PR 19-NOV-1999; 99US-0166678P.
PR 28-DEC-1999; 99US-0173396P.
PR 22-FEB-2000; 2000US-0184129P.
PR 28-FEB-2000; 2000US-0185421P.
PR 28-FEB-2000; 2000US-0185554P.
PR 02-MAR-2000; 2000US-0186530P.
PR 03-MAR-2000; 2000US-0186811P.
PR 09-MAR-2000; 2000US-0188114P.
PR 17-MAR-2000; 2000US-0190310P.
PR 21-MAR-2000; 2000US-0190800P.
PR 20-APR-2000; 2000US-0198568P.
PR 02-MAY-2000; 2000US-0201190P.
PR 08-MAY-2000; 2000US-0203111P.
PR 25-MAY-2000; 2000US-0207094P.
XX
(PHAA ) PHARMACIA & UPJOHN CO.
XX
Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
WPI; 2001-389826/41.
P-PSDB; AAG80968.
XX
New G protein-coupled receptor (nPCR-X) and its encoding polynucleotide
useful for diagnosing and treating e.g. schizophrenia.
XX
Claim 4; Page 83; 261pp; English.
XX
The present invention relates to novel G protein-coupled receptors
(nPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
the coding sequence for one such G protein-coupled receptor. GPCRs are
also known as seven transmembrane receptors and function in signal
transduction. The nPCRx coding sequences are useful for screening a
human to diagnose a disorder affecting the brain or a genetic
predisposition, specifically schizophrenia. nPCRx are useful for
identifying compounds useful for treating schizophrenia. Detection of
nPCRx in a sample is useful as a diagnostic tool for diseases or
disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
CNS disorders, infections such as HIV-1, metabolic and cardiovascular
diseases, proliferative disorders and hormonal disorders. Modulators of
nPCRx activity have the utility for treating neurological disorders,
```

CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity  
CC disorder/attention deficit disorder), and neuronal disorders such as  
CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.  
CC Additional disorders include inflammatory conditions (e.g. Crohn's  
CC disease), rheumatoid arthritis, autoimmune disorders, cancers,  
CC respiratory ailments such as asthma, and inflammatory diseases e.g.  
XX inflammatory bowel disease

SQ Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 4; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCG 60  
DB 1 ATGTAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCG 60

QY 61 CTGCTCATGTGGCCCTTTGTGCTGGCGCCTAGGCAATGGGCTGCGCCCTGTGTGTTTC 120  
DB 61 CTGCTCATGTGGCCCTTTGTGCTGGCGCCTAGGCAATGGGCTGCGCCCTGTGTGTTTC 120

QY 121 TGTTCACATGAAGACCTGGAGCCAGCAGCTGTTTACCTTTCAATTTGCGCGTGGCT 180  
DB 121 TGTTCACATGAAGACCTGGAGCCAGCAGCTGTTTACCTTTCAATTTGCGCGTGGCT 180

QY 181 GATTTCCCTCTATGATCTGCTGCTTTTCGACAGACTATTACTCAGACCTAGACAC 240  
DB 181 GATTTCCCTCTATGATCTGCTGCTTTTCGACAGACTATTACTCAGACCTAGACAC 240

QY 241 TGGGCTTTTGGGACATTCCTCCGCGAGTGGGGCTTTCACGTTGGCCATGAACAGGGCC 300  
DB 241 TGGGCTTTTGGGACATTCCTCCGCGAGTGGGGCTTTCACGTTGGCCATGAACAGGGCC 300

QY 301 GGGAGCATCGTGTCTTAACTGCTGGCTGGGAGAGTATTTCAAAGTGTCCACCCC 360  
DB 301 GGGAGCATCGTGTCTTAACTGCTGGCTGGGAGAGTATTTCAAAGTGTCCACCCC 360

QY 361 CACACGCGGTGAACATATCTCCACCGGGTGGGCTGCGATGCTGACCCCTGTGG 420  
DB 361 CACACGCGGTGAACATATCTCCACCGGGTGGGCTGCGATGCTGACCCCTGTGG 420

QY 421 GCGCTGGTCACTCTGGGAACTGTATCTTTTGTGGAGAACTCTCTGCTGCAAGAG 480  
DB 421 GCGCTGGTCACTCTGGGAACTGTATCTTTTGTGGAGAACTCTCTGCTGCAAGAG 480

QY 481 AGGCGGTCTCTGTGGAGCTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540  
DB 481 AGGCGGTCTCTGTGGAGCTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540

QY 541 TTCCAGCTGGAGTCTTTATGCCCCCTCGGCATCATCTTATTTTGTCTTCAAGATTGTT 600  
DB 541 TTCCAGCTGGAGTCTTTATGCCCCCTCGGCATCATCTTATTTTGTCTTCAAGATTGTT 600

QY 601 TGGAGCTGAGCGGAGGAGCAGCTGCGCCAGACAGGCTCGGATGAGAGGAGCCCG 660  
DB 601 TGGAGCTGAGCGGAGGAGCAGCTGCGCCAGACAGGCTCGGATGAGAGGAGCCCG 660

QY 661 TFCATCATGAGTGGTGGCAATGTTTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 720  
DB 661 TFCATCATGAGTGGTGGCAATGTTTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 720

QY 721 CTCTATTTCTCTGGAAGTGGCTCGAGTGGCTGCGATCCCTCTGCTCCATGGGCGCTG 780  
DB 721 CTCTATTTCTCTGGAAGTGGCTCGAGTGGCTGCGATCCCTCTGCTCCATGGGCGCTG 780

QY 781 CACATTAACCTCAGCTTACCTACATGAACAGCATGCTGGATCCCTCTGCTGATTTATTT 840  
DB 781 CACATTAACCTCAGCTTACCTACATGAACAGCATGCTGGATCCCTCTGCTGATTTATTT 840

QY 841 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTCTGAACCCAG 900  
DB 841 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTCTGAACCCAG 900

QY 901 CAGCCAGGACACTCAAAACACAAAGCCGAGAGATGCCAATTTCCAACTCTGGTCCG 960  
DB 901 CAGCCAGGACACTCAAAACACAAAGCCGAGAGATGCCAATTTCCAACTCTGGTCCG 960

QY 961 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGCTCTGATGGGCAATGGATCC 1020  
DB 961 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGCTCTGATGGGCAATGGATCC 1020

QY 1021 CACATTTGTGAGTGGCAC 1038  
DB 1021 CACATTTGTGAGTGGCAC 1038

RESULT 4  
AAS12581  
ID AAS12581 standard; cDNA; 1041 BP.  
XX  
AC AAS12581;  
DT 19-DEC-2001 (first entry)  
DE cDNA encoding novel human G protein-coupled receptor (GPCR).  
XX  
KW Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;  
hyperproliferative disorder; neurological disorder; psychiatric disease;  
inflammatory disorder; respiratory disorder; gene therapy; ss.  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS 1..1041  
FT /\*tag= a  
ET /product= "GPCR protein"  
XX  
WO200173029-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-US009522.  
XX  
PR 27-MAR-2000; 2000US-0192419P.  
PR 06-SEP-2000; 2000US-0230459P.  
PR 20-SEP-2000; 2000US-00666535.  
XX  
PA (PEXE ) PE CORP NY.  
XX  
PI Ye J, Cravchik A, Di Francesco V, Beasley EM;  
XX  
DR MPI; 2001-616503/71.  
XX  
PT Novel human G-protein coupled receptor proteins and nucleic acid  
PT molecules encoding the protein for use in developing human therapeutics  
PT and diagnostic compositions and for identifying modulators of the  
PT protein.  
XX  
PS Claim 23; Fig 1; 66pp; English.  
XX  
CC The present invention relates to the isolation of a novel human G-protein  
CC coupled receptor (GPCR) which is related to the chemokine receptor  
CC subfamily. The cDNA and gene sequences encoding for GPCR are also given  
CC in the invention. The sequences of the invention are useful for  
CC diagnosing and treating diseases or conditions mediated by human  
CC proteases. Such diseases include hyperproliferative disorders (e.g.  
hyperplasia), neurological disorders (e.g. Parkinson's disease),  
CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g.  
diabetes) and respiratory disorders (e.g. adult respiratory distress  
syndrome, ARDS). The GPCR protein is also useful for identifying a  
CC modulator of the expression of the protein. It also serves as a target  
CC for identifying agents for use in mammalian therapeutic applications,  
CC e.g. a human drug, particularly modulating a biological or pathological  
CC response in a cell or tissue that expresses the protein, in biological

assays related to GPCRs that are related to members of the chemokine receptor subfamily, in drug screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. The polynucleotide sequences can also be used in gene therapy. The present sequence encodes for the novel human GPCR of the invention

SQ Sequence 1041 B2; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 5; Length 1041;

Best Local Similarity 100.0%; Pred. No. 5e-287;

Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTAAACGGGTCTGTGTCGCGCATCGAGGGGAGACCACTCTCCAGGTGATCGCGCG 60

Db 1 ATGTAAACGGGTCTGTGTCGCGCATCGAGGGGAGACCACTCTCCAGGTGATCGCGCG 60

QY 61 CTGCTCATGTGGCCCTTGTGTGGCGGCACTAGGCAATGGGTGCGCTGTGTGTTTC 120

Db 61 CTGCTCATGTGGCCCTTGTGTGGCGGCACTAGGCAATGGGTGCGCTGTGTGTTTC 120

QY 121 TGTCTTCCACATGAAGACTGTGAAGCCAGCACTGTCTTTTCAATTTGGCCGTGGCT 180

Db 121 TGTCTTCCACATGAAGACTGTGAAGCCAGCACTGTCTTTTCAATTTGGCCGTGGCT 180

QY 181 GATTTCTCTTATGATCTGCTCTTTTGGACAGACTATTACTCAGAGCTAGACAC 240

Db 181 GATTTCTCTTATGATCTGCTCTTTTGGACAGACTATTACTCAGAGCTAGACAC 240

QY 241 TGGGCTTTTGGGCAATTCCTGCGAGTGGGCTTCTCAGTTGGCCATGAAGGGCC 300

Db 241 TGGGCTTTTGGGCAATTCCTGCGAGTGGGCTTCTCAGTTGGCCATGAAGGGCC 300

QY 301 GGGAGCATCGTTCCTTACGCTGTGCTGGGACAGTATTTCAAGGTGTCACCCC 360

Db 301 GGGAGCATCGTTCCTTACGCTGTGCTGGGACAGTATTTCAAGGTGTCACCCC 360

QY 361 CACACCGGTGAACATATCTCCACCGGTGGCGGTGGCATCTGTGCACCCCTGG 420

Db 361 CACACCGGTGAACATATCTCCACCGGTGGCGGTGGCATCTGTGCACCCCTGG 420

QY 421 GCCCTGCTCATCTGGGACAGTGTATCTTTTGTGGAGACCACTCTGGGTGCAAG 480

Db 421 GCCCTGCTCATCTGGGACAGTGTATCTTTTGTGGAGACCACTCTGGGTGCAAG 480

QY 481 ACGCCCTCTCTGTGAGCTTTCATCATGAGTGGGCAATGCTGGCATGACATG 540

Db 481 ACGCCCTCTCTGTGAGCTTTCATCATGAGTGGGCAATGCTGGCATGACATG 540

QY 541 TTCAGCTGAGTTCCTTATGCCCCCTGGCATCATCTTATTTTCTCTTCAAGATTGT 600

Db 541 TTCAGCTGAGTTCCTTATGCCCCCTGGCATCATCTTATTTTCTCTTCAAGATTGT 600

QY 601 TGGAGCTGAGGCGGAGCGAGCTGGCAGACAGGCTCGATGAGAGGCGACCCGG 660

Db 601 TGGAGCTGAGGCGGAGCGAGCTGGCAGACAGGCTCGATGAGAGGCGACCCGG 660

QY 661 TTCAATCATGTTGTGGCAATTTGTCTTACATGCTACCTGCGCAGCGTGTCTGCTAGA 720

Db 661 TTCAATCATGTTGTGGCAATTTGTCTTACATGCTACCTGCGCAGCGTGTCTGCTAGA 720

QY 721 CTCATTTCTCTGGAAGGTGCGCTCGAGTGGCTGGCATCCCTCTGCTGAGGGGCCCTG 780

Db 721 CTCATTTCTCTGGAAGGTGCGCTCGAGTGGCTGGCATCCCTCTGCTGAGGGGCCCTG 780

QY 781 CACATAACCTTCAGCTTCACTATACAGACAGTGTGGATCCCTGGTGTATTTT 840

Db 781 CACATAACCTTCAGCTTCACTATACAGACAGTGTGGATCCCTGGTGTATTTT 840

QY 841 TCAAGCCCTCTCTTTTCCCAATTTCTACAACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900

Db 841 TCAAGCCCTCTCTTTTCCCAATTTCTACAACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900

QY 901 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGATGCCAATTTTCGAACTCGGTCCG 960

Db 901 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGATGCCAATTTTCGAACTCGGTCCG 960

QY 961 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTCTGATGGGCAATGGGATCCC 1020

Db 961 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTCTGATGGGCAATGGGATCCC 1020

QY 1021 CACATTGTGAGTGGCAC 1038

Db 1021 CACATTGTGAGTGGCAC 1038

#### RESULT 5

AAS07946

ID AAS07946 standard; cDNA; 1041 BP.

XX AAS07946;

XX AC

XX XX

DT 23-OCT-2001 (first entry)

XX Human cDNA encoding G-protein coupled receptor, hRUP19.

DE Human; G-protein coupled receptor; GPCR; hRUP19; agonist;

KW inverse agonist; lung cancer; ss.

XX Homo sapiens.

OS

XX Key

FT CDS

FT Location/Qualifiers

FT 1..1041

FT /\*tag= a

FT /product= "hRUP19"

XX WO200136471-A2.

PN

XX 25-MAY-2001.

PD

PF 16-NOV-2000; 2000WO-US031509.

XX

XX 17-NOV-1999; 99US-0166088P.

PR 17-NOV-1999; 99US-0166099P.

PR 17-NOV-1999; 99US-0166369P.

PR 23-DEC-1999; 99US-0171900P.

PR 23-DEC-1999; 99US-0171901P.

PR 23-DEC-1999; 99US-0171902P.

PR 11-FEB-2000; 2000US-0181749P.

PR 14-MAR-2000; 2000US-0189258P.

PR 14-MAR-2000; 2000US-0189259P.

PR 10-APR-2000; 2000US-0195898P.

PR 10-APR-2000; 2000US-0195899P.

PR 10-APR-2000; 2000US-0196078P.

PR 28-APR-2000; 2000US-0200419P.

PR 12-MAY-2000; 2000US-0203630P.

PR 12-JUN-2000; 2000US-0210741P.

PR 12-JUN-2000; 2000US-0210982P.

PR 21-AUG-2000; 2000US-0226760P.

PR 26-SEP-2000; 2000US-0235418P.

PR 26-SEP-2000; 2000US-0235418P.

PR 20-OCT-2000; 2000US-0242332P.

PR 20-OCT-2000; 2000US-0242332P.

PR 24-OCT-2000; 2000US-0243019P.

XX (AREN-) ARENA PHARM INC.

XX

XX Chen R, Dang HT, Lowitz KP;

XX WPI; 2001-355616/37.

DR P-PSDB; AAU04373.

XX Endogenous and non-endogenous versions of human G-protein coupled

PT receptors for direct identification of candidate compounds as agonists,

PT inverse agonists or partial agonists for use as therapeutic agents.

XX

PS Claim 47; Page 115; 160pp; English.

XX The sequence encodes a human G-protein coupled receptor (GPCR), hRUP19

CC The endogenous and non-endogenous, constitutively activated versions of

CC human G-protein coupled receptors (GPCR), are useful for direct

CC identification of candidate compounds as receptor agonists, inverse

CC agonists or partial agonists having applicability as therapeutic agents

CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous

CC version of human GPCRs are also utilized in research settings and in

CC vitro and in vivo system, incorporating GPCRs can be utilized to

CC elucidate and understand the roles these receptors play in the human

CC condition, both normal and diseased

XX

SQ Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 5; Length 1041;

Best Local Similarity 100.0%; Pred. No. 5e-287;

Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACAAGGTCGTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60

DB 2 ATGTACAAGGTCGTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60

QY 61 CTGCTCAATGTGCGCTTGTGTGGCGCACTAGGCAATGGGCTCGCCCTGTGTGTTTC 120

DB 61 CTGCTCAATGTGCGCTTGTGTGGCGCACTAGGCAATGGGCTCGCCCTGTGTGTTTC 120

QY 121 TGTCTCCACATGAAGACCTGGAGCCGACGACCTGTTTACCTTTCAATTTGGCGTGGCT 180

DB 121 TGTCTCCACATGAAGACCTGGAGCCGACGACCTGTTTACCTTTCAATTTGGCGTGGCT 180

QY 181 GATTTCTCTATGATCTGCTGCTGCTTTCGACAGACATTTACCTCAGACCTAGACAC 240

DB 181 GATTTCTCTATGATCTGCTGCTGCTTTCGACAGACATTTACCTCAGACCTAGACAC 240

QY 241 TGGGCTTTTGGGACATTCCTCGGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 300

DB 241 TGGGCTTTTGGGACATTCCTCGGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 300

QY 301 GGGAGCATGCTGTCTTACCGTGGTGGCTGGGACAGGTATTTCAAGTGGTCCACCC 360

DB 301 GGGAGCATGCTGTCTTACCGTGGTGGCTGGGACAGGTATTTCAAGTGGTCCACCC 360

QY 361 CACGAGCGGTGAACATCTATCCACCGGCTGGGCTGGGATGCTGCTGACCTGTGG 420

DB 361 CACGAGCGGTGAACATCTATCCACCGGCTGGGCTGGGATGCTGCTGACCTGTGG 420

QY 421 GCGCTGGTCACTCTGGGACAGTGTATCTTTTCTGGAGAACCATCTTGGCGTGAAGAG 480

DB 421 GCGCTGGTCACTCTGGGACAGTGTATCTTTTCTGGAGAACCATCTTGGCGTGAAGAG 480

QY 481 AGGGCGCTCTCTGAGAGCTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540

DB 481 AGGGCGCTCTCTGAGAGCTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540

QY 541 TCCAGCTGGAGTTCCTTATGCGCCCTCGGATCATCTTATTTTGTCTCTTCAAGATTGT 600

DB 541 TCCAGCTGGAGTTCCTTATGCGCCCTCGGATCATCTTATTTTGTCTCTTCAAGATTGT 600

QY 601 TGGAGCTTGAAGCGGAGGACAGCTGGCCAGACAGGCTCGATGAAGAGGCGACCGG 660

DB 601 TGGAGCTTGAAGCGGAGGACAGCTGGCCAGACAGGCTCGATGAAGAGGCGACCGG 660

QY 661 TCCATCATGCTGGTGGCAATGTGTTTATCATGCTTACCTGCGGCTGCTGCTGCTAGA 720

DB 661 TCCATCATGCTGGTGGCAATGTGTTTATCATGCTTACCTGCGGCTGCTGCTGCTAGA 720

QY 721 CTCTATTCTCTGGAGCGGCTCGAGTGGCTGCGATCCCTCTCTGTCATGGGCGCTG 780

DB 721 CTCTATTCTCTGGAGCGGCTCGAGTGGCTGCGATCCCTCTCTGTCATGGGCGCTG 780

QY 781 CACATAACCTCAGCTTCACCTACATGAACAGCATGCTGATCCCTGCTGTATTATTTT 840

DB 781 CACATAACCTCAGCTTCACCTACATGAACAGCATGCTGATCCCTGCTGTATTATTTT 840

QY 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAGCTCAAAATCTGCAGTCTGAACCCAG 900

DB 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAGCTCAAAATCTGCAGTCTGAACCCAG 900

QY 901 CAGCCAGGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTGGAACCTCGGTGCG 960

DB 901 CAGCCAGGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTGGAACCTCGGTGCG 960

QY 961 AGGAGTTGATCAGTGTGGCAAAATAGTTTCCAAAGCAGTCTGATGGGCAATGGATCCC 1020

DB 961 AGGAGTTGATCAGTGTGGCAAAATAGTTTCCAAAGCAGTCTGATGGGCAATGGATCCC 1020

QY 1021 CACATTGTTGAGTGGCAC 1038

DB 1021 CACATTGTTGAGTGGCAC 1038

RESULT 6

AAD27497

ID AAD27497 standard; DNA; 1041 BP.

XX

AC AAD27497;

XX

DT 18-APR-2002 (first entry)

XX

DE Human G-protein coupled receptor (GPCRx14) DNA.

XX

XX Human; G-protein coupled receptor; GPCRx14; cerebroprotective; vomiting;

KW receptor-mediated disorder; therapy; urinary retention; allergy; obesity;

KW osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;

KW anorexia; tumor; migraine; acute heart failure; ulcer; antiinflammatory;

KW stroke; hypertension; neuronal disorder; myocardial infarction; psychiatric;

KW depression; mental retardation; neurodegenerative disease; antibacterial;

KW Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;

KW Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;

KW vulnarary; analgesic; anorectic; diuretic; cardiac; nootropic;

KW antiemetic; vasotropic; diabetes; cancer; tranquilizer; neuroleptic; ds.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT 1.1041

CDS /\*tag= a

FT /product= "Human GPCRx14 protein"

FT

XX

XX WO200198330-A2.

XX

XX 27-DEC-2001.

XX

XX 20-JUN-2001; 2001WO-BRD00104.

XX

XX 20-JUN-2000; 2000US-0212913P.

PR 11-JUL-2000; 2000US-0217494P.

PR 26-JAN-2001; 2001EP-00870015.

PR 12-FEB-2001; 2001EP-00870024.

XX

XX (EURO-) EUROSCHEN SA.

XX

XX Lannoy V, Brezillon S, Dethaux M, Parmentier M, Govarts C;

PI

XX

XX WPI; 2002-130789/17.

XX

XX P-PSDB; AAE17077.

DR

DR

XX

XX New G-protein coupled receptor, useful in the manufacture of medicaments

PT for treating receptor mediated disorders e.g. acute heart failure and

PT Alzheimer's disease.

XX

XX Example 2; Page 28-29; 46pp; English.

XX

XX The present invention relates to a G-protein coupled receptor (GPCR) and

CC nucleotide encoding it. GPCR are useful in the manufacture of a



medicament for the prevention and/or treatment of receptor-mediated disorders e.g. viral infections, virus and bacterial diseases, diseases and disorders involving disturbances of cell migration, diseases or perturbations of immune system including cancers, development of tumours and tumour metastasis, inflammatory and neoplastic processes; bacterial and fungal infections, in wound and bone healing, dysfunction of regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia, urinary retention, osteoporosis, angina pectoris, atherosclerosis, restenosis, diseases involving excessive or reduced proliferation or loss of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting; blood circulating affections including acute heart failure, hypertension, hypertension and myocardial infarction; psychotic; neuronal disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, severe mental retardation; degenerative diseases; neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g. Huntington's disease or Gilles de la Tourette's syndrome and other related diseases. The present sequence is GPCR14 DNA

XX Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 6; Length 1041;  
 Best Local Similarity 100.0%; Pred. No. 5e-287;  
 Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTACAAAGCGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
 1 ATGTACAAAGCGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60

61 CTGCTCATTTGTGGCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTTTC 120  
 61 CTGCTCATTTGTGGCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTTTC 120

121 TGCTTCACATGAGACCTGGAACCCAGCAGCTGTTTACCTTTTCAATTTGGCGTGGCT 180  
 121 TGCTTCACATGAGACCTGGAACCCAGCAGCTGTTTACCTTTTCAATTTGGCGTGGCT 180

181 GAATTCCTCTTATGATCTGCTGCTCTTTTCGGACAGACTATACCTCAGACGTAGACAC 240  
 181 GAATTCCTCTTATGATCTGCTGCTCTTTTCGGACAGACTATACCTCAGACGTAGACAC 240

241 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGGCTTTCAGTTGGCCATGAACAGGGCC 300  
 241 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGGCTTTCAGTTGGCCATGAACAGGGCC 300

301 GGGAGCATGCTGTCTTACGTTGGTGGCTGCGACAGGATTTTCAAGTGGTCCACCCC 360  
 301 GGGAGCATGCTGTCTTACGTTGGTGGCTGCGACAGGATTTTCAAGTGGTCCACCCC 360

361 CACACGCGGTGAACACTATCTCCACCCGGGTGGCGCTGGCATCTGTCACCCCTGTGG 420  
 361 CACACGCGGTGAACACTATCTCCACCCGGGTGGCGCTGGCATCTGTCACCCCTGTGG 420

421 GCCCTGGTGTACTCTGGAAACAGTGTATCTTTTGTGAGAACCAATCTGCTGCAAGAG 480  
 421 GCCCTGGTGTACTCTGGAAACAGTGTATCTTTTGTGAGAACCAATCTCTGCTGCAAGAG 480

481 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTCCGCAATGCTGGCATGACATCATG 540  
 481 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTCCGCAATGCTGGCATGACATCATG 540

541 TTCAGCTGGAGTTCTTTATGCCCTCGGCATCATCTTATTTTGTCTCTTCAAGATTGTT 600  
 541 TTCAGCTGGAGTTCTTTATGCCCTCGGCATCATCTTATTTTGTCTCTTCAAGATTGTT 600

601 TGGAGCTTGGGAGGAGGAGAGCTGGCCAGACAGGCTGGATGAAGAAGGCGACCCGG 660  
 601 TGGAGCTTGGGAGGAGGAGAGCTGGCCAGACAGGCTGGATGAAGAAGGCGACCCGG 660

661 TTCAATCATGTTGGTGGCAATTTGTTTTCATCATGCTTACCTGCCCGGCTCTGTGAGA 720  
 661 TTCAATCATGTTGGTGGCAATTTGTTTTCATCATGCTTACCTGCCCGGCTCTGTGAGA 720

721 CTCATATTCCTCTGAGCGGTGCCCTCGAGTGCCTCGATCCCTCTGTCTCATGGGCCCTG 780  
 721 CTCATATTCCTCTGAGCGGTGCCCTCGAGTGCCTCGATCCCTCTGTCTCATGGGCCCTG 780

781 CACATAACCTTCAGCTTACCTCATGATGAACAGCATGTGTGGATCCCTGGTGTATTATTT 840  
 781 CACATAACCTTCAGCTTACCTCATGATGAACAGCATGTGTGGATCCCTGGTGTATTATTT 840

841 TCAGAGCCCTCTCTTCCCAATTCACACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900  
 841 TCAGAGCCCTCTCTTCCCAATTCACACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900

901 CAGCAGGACACTCAAAAACACAAAGCCGGAAGATGCCAATTTGCAACCTCGTGGC 960  
 901 CAGCAGGACACTCAAAAACACAAAGCCGGAAGATGCCAATTTGCAACCTCGTGGC 960

961 AGGAGTTGCACTAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGCAATGGGATCCC 1020  
 961 AGGAGTTGCACTAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGCAATGGGATCCC 1020

1021 CACATTTGTGAGTGGCAC 1038  
 1021 CACATTTGTGAGTGGCAC 1038

RESULT 7  
 ABS70241  
 ID ABS70241 standard; DNA; 1041 BP.  
 XX  
 XX ABS70241;  
 XX 26-NOV-2002 (first entry)  
 XX  
 XX DNA encoding human G protein-coupled receptor, nGPCR-11.  
 XX Human; gene; ds; G protein-coupled receptor; GPCR; nGPCR; besPCR;  
 KW nG protein coupled receptor; communication; serpentine structure;  
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;  
 KW genetic predisposition; brain; immune response; gene therapy;  
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;  
 KW Huntington's disease; dyskinesia; manic depression; stroke;  
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;  
 KW tranquiliser.  
 XX Homo sapiens.  
 XX WO200264789-Al.  
 XX 22-AUG-2002.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 XX Lind P, Parodi LA, Vogeli G, Wood LS;  
 XX WPI; 2002-674879/72.  
 XX P-PSDB; ABG93786.  
 XX  
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,  
 PT useful for treating or diagnosing a mental disorder or a disorder  
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or  
 PT Parkinson's disease.  
 XX  
 XX Example 1; Page 84; 244pp; English.  
 XX  
 XX The invention discloses an isolated human polypeptide, and encoding  
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the  
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the  
 CC communication between cells and their environment and are characterised  
 CC by a serpentine structure that passes through the cell membrane seven

CC times, hence the reason such receptors are sometimes called seven  
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are  
CC useful for identifying an nGPR allelic variant that correlates with a  
CC mental disorder, for isolating an antibody that binds to an epitope of  
CC the polypeptide, and/or identifying a compound that binds the polypeptide or  
CC polynucleotide and/or modulates its biological activity, for screening a  
CC human subject to diagnose a disorder, or a genetic predisposition to a  
CC disorder, affecting the brain or a genetic disposition to the disorder,  
CC for identifying compounds useful for the treatment of a mental disorder  
CC and for identifying a compound useful as a modulator of binding between  
CC nGPR-14 and a binding partner of nGPR-14. The polypeptide is also  
CC useful for inducing an immune response in a mammal. The nucleic acid or  
CC polypeptide is particularly useful, using gene therapy, for treating e.g.  
CC anxiety disorders, depression, bipolar disorder, schizophrenia,  
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's  
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also  
CC be used for treating diabetes, inflammation or wounds. The sequences  
CC presented in ABS70202-ABS70248, ABS70338 and ABS70243 are the DNAs  
CC encoding the nGPRs (also referred to as beGPRs)

XX SQ Sequence 1041 BP; 208 A; 234 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 6; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTCTGTGCGGCATCGAGGGGACACATCTCCAGGTGATGCCGG 60  
DB |||||  
QY 1 ATGTACACGGGTCTGTGCGGCATCGAGGGGACACATCTCCAGGTGATGCCGG 60  
DB |||||  
QY 61 CTGCTCATGTGGGCTTTGTGCTGGCGCATAGGCAATGGGGTGGCCCTGTGTGTTTC 120  
DB |||||  
QY 61 CTGCTCATGTGGGCTTTGTGCTGGCGCATAGGCAATGGGGTGGCCCTGTGTGTTTC 120  
DB |||||  
QY 121 TGGTTCACATGAGACCTCGAAGCCAGCCAGCTGTGTACCTTTTCAATTTGGCCGTGCT 180  
DB |||||  
QY 121 TGGTTCACATGAGACCTCGAAGCCAGCCAGCTGTGTACCTTTTCAATTTGGCCGTGCT 180  
DB |||||  
QY 181 GATTTCTCTTTATGATCTGCTGCTGCTTTTGGGACAGACTATTACTCAGACGTAGAC 240  
DB |||||  
QY 181 GATTTCTCTTTATGATCTGCTGCTGCTTTTGGGACAGACTATTACTCAGACGTAGAC 240  
DB |||||  
QY 241 TGGGCTTTTGGGACATTCCTTCCGAGTGGGGCTTTTTCAGTTTGGCCATGAACAGGGCC 300  
DB |||||  
QY 241 TGGGCTTTTGGGACATTCCTTCCGAGTGGGGCTTTTTCAGTTTGGCCATGAACAGGGCC 300  
DB |||||  
QY 301 GGGAGATCGTGTCTTCAAGTGTGTGCTGCGGACAGGTATTTCAAAAGTGTCCACCC 360  
DB |||||  
QY 301 GGGAGATCGTGTCTTCAAGTGTGTGCTGCGGACAGGTATTTCAAAAGTGTCCACCC 360  
DB |||||  
QY 361 CACACCGGTGAAACACTATCTCACCCGGGTGGCGGCTGGCATCTGTCACCCCTGTGG 420  
DB |||||  
QY 361 CACACCGGTGAAACACTATCTCACCCGGGTGGCGGCTGGCATCTGTCACCCCTGTGG 420  
DB |||||  
QY 421 GCGCTGCTCATCTGGGACAGTGTATCTTTTGGTGGAGAACCACTCTCTGGTGAACAG 480  
DB |||||  
QY 421 GCGCTGCTCATCTGGGACAGTGTATCTTTTGGTGGAGAACCACTCTCTGGTGAACAG 480  
DB |||||  
QY 481 ACGGCGTCTCTGTGAGAGCTTATCATGAGTGGCCATAGGCTGGCATGACATCATG 540  
DB |||||  
QY 481 ACGGCGTCTCTGTGAGAGCTTATCATGAGTGGCCATAGGCTGGCATGACATCATG 540  
DB |||||  
QY 541 TCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTATTTGCTCTCAAGATTCTT 600  
DB |||||  
QY 541 TCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTATTTGCTCTCAAGATTCTT 600  
DB |||||  
QY 601 TGGAGCTTGAAGCGGAGCAGCTGCGCCAGACAGAGCTCGGATGAAGAGCGACCCGG 660  
DB |||||  
QY 601 TGGAGCTTGAAGCGGAGCAGCTGCGCCAGACAGAGCTCGGATGAAGAGCGACCCGG 660  
DB |||||  
QY 661 TTCTATCATGTTGGGCAATTTGTGTTTATCATGCTACCTGCGCCAGGCTGTCTGCTAGA 720  
DB |||||  
QY 661 TTCTATCATGTTGGGCAATTTGTGTTTATCATGCTACCTGCGCCAGGCTGTCTGCTAGA 720  
DB |||||

QY 721 CTCTATTTCTTGGACGGTGGCCCTCGAGTGGCTGGATCCCTCTGTCCATGGGGCCCTG 780  
DB |||||  
QY 721 CTCTATTTCTTGGACGGTGGCCCTCGAGTGGCTGGATCCCTCTGTCCATGGGGCCCTG 780  
DB |||||  
QY 781 CACATAACCCCTCAGCTTCCACCTACATGAACAGCATGCTGGATCCCTCTGTGTATTATTTT 840  
DB |||||  
QY 781 CACATAACCCCTCAGCTTCCACCTACATGAACAGCATGCTGGATCCCTCTGTGTATTATTTT 840  
DB |||||  
QY 841 TCAAGCCCTCTCTTTCCCAAAATTTCAACACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900  
DB |||||  
QY 841 TCAAGCCCTCTCTTTCCCAAAATTTCAACACAGCTCAAAATCTGCAGTCTGAACCCCAAG 900  
DB |||||  
QY 901 CAGCAGGACACTCAAAACACAAAGGCGGAGAGATGSCCAATTTCCGAACCTCGGTGCG 960  
DB |||||  
QY 901 CAGCAGGACACTCAAAACACAAAGGCGGAGAGATGSCCAATTTCCGAACCTCGGTGCG 960  
DB |||||  
QY 961 AGGAGTTGCATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020  
DB |||||  
QY 961 AGGAGTTGCATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020  
DB |||||  
QY 1021 CACATTGTTGAGTGGCAC 1038  
DB |||||  
QY 1021 CACATTGTTGAGTGGCAC 1038  
DB |||||  
RESULT 8  
ABZ42873  
ID ABZ42873 standard; DNA; 1041 BP.  
XX AC ABZ42873;  
XX DT 06-MAR-2003 (first entry)  
XX DE Human GPCR polynucleotide SEQ ID NO 7.  
XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
XX KW drug development; gustatory; taste; fragrance; gene; ds.  
XX OS Homo sapiens.  
XX PN WO200216548-A2.  
XX PD 28-FEB-2002.  
XX PF 30-JUL-2001; 2001WO-IB001446.  
XX PR 04-AUG-2000; 2000JP-00237818.  
XX PR 13-FEB-2001; 2001JP-00034434.  
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX PI Haga T, Takeda S, Mitaku S;  
XX WPI; 2002-304118/34.  
XX P-PSDB; ABP95599.  
XX Database global search for G protein-coupled receptors, proteins and  
XX encoded genes for studying in vivo signal transduction mechanism and  
XX identifying targets for drug development.  
XX Claim 9; SEQ ID NO 7; 97pp + Sequence Listing; Japanese.  
XX The invention relates to a method for screening G protein-coupled  
XX receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-  
XX ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
XX domains with 250-1000 amino acid residues to give a gene homologous with  
XX a known GPCR gene. The receptor proteins and encoded genes are useful for  
XX studying in vivo signal transduction mechanism and identifying targets  
XX for drug development e.g. based on olfactory and gustatory receptors in  
XX form of agonists and antagonists by screening intrinsic and extrinsic  
XX ligands as bitter taste inhibitors, taste enhancers and fragrance  
XX improvers. Note: The sequence data for this patent did not form part of



CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Query Match 100.0%; Score 1038; DB 6; Length 1041;  
XX Best Local Similarity 100.0%; Pred. No. 5e-287;

SQ Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACAAAGCGGTGCTGTGCGCATCGAGGGGAGACCATCTCCAGGTTGATGCGCGG 60  
DB 1 ATGTACAAAGCGGTGCTGTGCGCATCGAGGGGAGACCATCTCCAGGTTGATGCGCGG 60  
QY 61 CTGCTCATTTGGGCTTTGCTGGGCGCACTAGGCAATGGGTCGCCCTGNGTGTTTC 120  
DB 61 CTGCTCATTTGGGCTTTGCTGGGCGCACTAGGCAATGGGTCGCCCTGNGTGTTTC 120  
QY 121 TGCTTCCACATGAAGACCTGGAAGCCAGACACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
DB 121 TGCTTCCACATGAAGACCTGGAAGCCAGACACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
QY 181 GATTTCCCTTATGATCTGCTGCTTTTCCGACAGACTATTTACCTTTTCAATTTGGCCGTGGCT 240  
DB 181 GATTTCCCTTATGATCTGCTGCTTTTCCGACAGACTATTTACCTTTTCAATTTGGCCGTGGCT 240  
QY 241 TGGGCTTTTGGGGACATTTCCCTGCGGCTGCGGCTCTTTCAGCTTGGCCATGAACAGGCCC 300  
DB 241 TGGGCTTTTGGGGACATTTCCCTGCGGCTGCGGCTCTTTCAGCTTGGCCATGAACAGGCCC 300  
QY 301 GGGAGCATGTTGTTCTTTACGGTGGTGGCTGCGACAGGTATTTCAAAGTGTGTCACCC 360  
DB 301 GGGAGCATGTTGTTCTTTACGGTGGTGGCTGCGACAGGTATTTCAAAGTGTGTCACCC 360  
QY 361 CACACAGGCTGAACACTATCTTCCACCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 420  
DB 361 CACACAGGCTGAACACTATCTTCCACCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 420  
QY 421 GCCCTGGTCTATCTGCGGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCTGTCGAGAG 480  
DB 421 GCCCTGGTCTATCTGCGGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCTGTCGAGAG 480  
QY 481 ACGGCGGTCTCTGCTGAGAGCTTCATCATGAGTGGCCCAATGGCTGGCATGACATCATG 540  
DB 481 ACGGCGGTCTCTGCTGAGAGCTTCATCATGAGTGGCCCAATGGCTGGCATGACATCATG 540  
QY 541 TTCCAGCTGGAGTTCTTTATGCCCTCTGGCATCATCTTATTTGCTCTTCAAGATTGTT 600  
DB 541 TTCCAGCTGGAGTTCTTTATGCCCTCTGGCATCATCTTATTTGCTCTTCAAGATTGTT 600  
QY 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAGAGGCGGACCCGG 660  
DB 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAGAGGCGGACCCGG 660  
QY 661 TTATCATGTTGGTGGCAATTTGTTTTCATCATGCTACCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 TTATCATGTTGGTGGCAATTTGTTTTCATCATGCTACCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 CTCTATTTCTCTGGAAGGCTGCTGAGTGGCTGCGATCCCTCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 CTCTATTTCTCTGGAAGGCTGCTGAGTGGCTGCGATCCCTCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 CACATACCTCTCAGCTTTCACCTACATGAACAGCATGCTGGATCCCTCTGCTGCTGCTGCTG 840  
DB 781 CACATACCTCTCAGCTTTCACCTACATGAACAGCATGCTGGATCCCTCTGCTGCTGCTGCTG 840  
QY 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAGCTCAAAATCTCAGTCTGAAACCCCAAG 900  
DB 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAGCTCAAAATCTCAGTCTGAAACCCCAAG 900  
QY 901 CAGCCAGGACACTCAAAAACACAAAGCGCGGAGAGATGCCAATTTTGAACCTCGTGGCG 960  
DB 901 CAGCCAGGACACTCAAAAACACAAAGCGCGGAGAGATGCCAATTTTGAACCTCGTGGCG 960

QY 961 AGGAGTTCATCAGTGTGCAAAATAGTTTCCAAAGCCAGTCTGTGATGGCAATGGGATCCC 1020  
DB 961 AGGAGTTCATCAGTGTGCAAAATAGTTTCCAAAGCCAGTCTGTGATGGCAATGGGATCCC 1020

QY 1021 CACATTGTTGAGTGGCAC 1038  
DB 1021 CACATTGTTGAGTGGCAC 1038

RESULT 9  
AAL42499  
ID AAL42499 standard; DNA; 1041 BP.  
XX  
AC AAL42499;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Human purinergic-like G-protein coupled receptor (AXOR87) DNA sequence.  
XX  
KW Human; gene; ds; purinergic-like G-protein coupled receptor; AXOR87;  
KW immunity; autoimmunity; inflammation; immunodeficiency;  
KW bacterial infection; fungal infection; viral infection;  
KW protozoa infection; cancer; diabetes; obesity; anorexia; bulimia; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis; psychotic disorder;  
KW neurological disorder; vaccine; chromosome 12q24.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
CDS 1..1041  
FT /\*tag= a  
FT /product= "Human purinergic-like G-protein coupled  
FT receptor AXOR87"

FN GB2365868-A.

XX 27-FEB-2002.

XX 25-MAY-2001; 2001GB-00012860.

XX 30-NOV-2000; 2000US-00590675.

PR 02-NOV-2000; 2000GB-00026839.

XX (SMIX ) SMITHKLINE BEECHAM CORP.

XX (SMIX ) SMITHKLINE BEECHAM PLC.

XX (GLAX ) GLAXO GROUP LTD.

XX Ignar DM, Eishourbagy N, Gattu M, Shabon U;

XX WPI; 2002-364852/40.

XX P-PSDB; AAO14788.

XX New purinergic-like G-protein coupled receptor AXOR87 polypeptide and  
XX polynucleotide, useful for treating diseases related to autoimmunity,  
XX inflammation, immunodeficiency, or bacterial, fungal, viral and protozoal  
XX infections.

XX Claim 5; Page 36; 47pp; English.

XX The invention comprises the amino acid and coding sequence of the human  
XX purinergic-like G-protein coupled receptor AXOR87. The AXOR87 DNA and  
XX protein sequences of the invention may be used for treating diseases  
XX related to immunity, autoimmunity, inflammation, immunodeficiency, and  
XX infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and  
XX protein sequences are particularly useful for treating: cancers,  
XX diabetes, obesity, anorexia, bulimia, psoriasis, asthma, rheumatoid  
XX arthritis, osteoarthritis, as well as psychotic and neurological  
XX disorders. The AXOR87 DNA and protein sequences may also be used as  
XX vaccines. The present DNA sequence (located on chromosome 12q24) encodes  
XX the human AXOR87 protein

XX Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 6; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

QY 1 ATGTACAAACGGTCTGCTGCGCATCGAGGGGACACCATCTCCAGGGTGAATCCCGCG 60  
DB 1 ATGTACAAACGGTCTGCTGCGCATCGAGGGGACACCATCTCCAGGGTGAATCCCGCG 60

QY 61 CTGCTCATTTGGGCTTTTGTGCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 120  
DB 61 CTGCTCATTTGGGCTTTTGTGCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 120

QY 121 TGGCTTCCATGAAGACCTGGAGCCCGCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
DB 121 TGGCTTCCATGAAGACCTGGAGCCCGCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180

QY 181 GATTTCCTCTTATGATCTGCTGCTGCTTTTGGACAGACATATTACCTCAGACGTAGACAC 240  
DB 181 GATTTCCTCTTATGATCTGCTGCTGCTTTTGGACAGACATATTACCTCAGACGTAGACAC 240

QY 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGGCTCTTACGTTGGCCATGAACAGGGCC 300  
DB 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGGCTCTTACGTTGGCCATGAACAGGGCC 300

QY 301 GGGAGCATCGTGTTCCTTACCGTGGTGGCTGCGACAGGTATTTCAAAGTGGTCCACCCC 360  
DB 301 GGGAGCATCGTGTTCCTTACCGTGGTGGCTGCGACAGGTATTTCAAAGTGGTCCACCCC 360

QY 361 CACACGCGGTGAACATATCTCCACCGGGTGGCGGCTGGCATGCTGCTGACCTGTGG 420  
DB 361 CACACGCGGTGAACATATCTCCACCGGGTGGCGGCTGGCATGCTGCTGACCTGTGG 420

QY 421 GCGCTGGTCACTCTGGGAAACAGTGTATCTTTGCTGGAGAACCATCTCTCGGTGCAAGAG 480  
DB 421 GCGCTGGTCACTCTGGGAAACAGTGTATCTTTGCTGGAGAACCATCTCTCGGTGCAAGAG 480

QY 481 AGGCGCGTCTCTGTGAGAGCTTTCATGAGTGGGCGCCAAATGCTGGCATGATCATG 540  
DB 481 AGGCGCGTCTCTGTGAGAGCTTTCATGAGTGGGCGCCAAATGCTGGCATGATCATG 540

QY 541 TTCCAGCTGGAGTTCTTTATGCGCTTGGCATCATCTTATTTTCTCTCTCAGATTGTT 600  
DB 541 TTCCAGCTGGAGTTCTTTATGCGCTTGGCATCATCTTATTTTCTCTCTCAGATTGTT 600

QY 601 TGGAGCCTTGAAGCGGAGCAGCAGCTGGCCAGACAGGCTCGATGAAGAGGCGCCCG 660  
DB 601 TGGAGCCTTGAAGCGGAGCAGCAGCTGGCCAGACAGGCTCGATGAAGAGGCGCCCG 660

QY 661 TTCCATCATGGTGGCAATTTGTTTCATCATGCTACTGTCGCCAGCGTGTCTGTAGA 720  
DB 661 TTCCATCATGGTGGCAATTTGTTTCATCATGCTACTGTCGCCAGCGTGTCTGTAGA 720

QY 721 CTCTATTTCTTGAAGCGTGGCTCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 CTCTATTTCTTGAAGCGTGGCTCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 TCAGCGCCCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGTGAACCCCAAG 900  
DB 841 TCAGCGCCCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGTGAACCCCAAG 900

QY 901 CAGCCAGGACACTCAAAACACAAAGCCGAGAGATGCCAATTTTCGAACCTCGTCCG 960  
DB 901 CAGCCAGGACACTCAAAACACAAAGCCGAGAGATGCCAATTTTCGAACCTCGTCCG 960

QY 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGATCCC 1020  
DB 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGATCCC 1020

QY 1021 CACATTGTTGAGTGGCAC 1038

DB 1021 CACATTGTTGAGTGGCAC 1038

RESULT 10  
AB222648  
ID AB222648 standard; cDNA; 1041 BP.  
XX  
AC AB222648;  
XX  
DT 31-MAR-2003 (first entry)  
XX  
Human GAVE3 encoding cDNA SEQ ID NO:1.  
XX  
Human; GAVE3; G protein-coupled receptor; GPCR; antiinflammatory;  
XX  
antialsthmatic; antirheumatic; antiarthritic; inflammatory disorder;  
XX  
asthma; chronic obstructive pulmonary disease; rheumatoid arthritis;  
XX  
chromosome 12; gene; ss.  
XX  
Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS 1..1041  
FT /\*tag= a  
FT /product= "GAVE3"  
FT /note= "G protein-coupled receptor (GPCR)"  
XX  
PN W02003000846-A2.  
XX  
XX 03-JAN-2003.  
XX  
XX 21-JUN-2002; 2002WO-US019490.  
XX  
XX 22-JUN-2001; 2001US-00886041.  
XX  
XX (AVET ) AVENTIS PHARM INC.  
XX  
XX Xia T, Ni D, Bishindrelo H, Ardati A, Minnich A, Jupp R;  
XX WPI; 2003-184040/18.  
XX P-PSDB; ABP56751.  
XX  
XX New GAVE3 nucleic acid and polypeptide, for preventing or treating a  
XX disorder associated with aberrant GAVE3 expression or activity, e.g.  
XX inflammatory disease, asthma, chronic obstructive pulmonary disease or  
XX rheumatoid arthritis.  
XX  
XX Claim 1; Fig 1; 90pp; English.  
XX  
XX The present sequence encodes a human G protein-coupled receptor (GPCR),  
XX designated GAVE3. GAVE3 is located on human chromosome 12. GAVE3 has  
XX antiinflammatory, antialsthmatic, antirheumatic and antiarthritic  
XX activities. GAVE3 nucleic acids, polypeptides, agonists and antagonists  
XX can be used for preventing or treating a disorder associated with  
XX aberrant GAVE3 expression or activity, e.g. inflammatory disorders such  
XX as asthma, chronic obstructive pulmonary disease or rheumatoid arthritis.  
XX The nucleic acids and polypeptides can also be useful for identifying  
XX modulators, i.e. candidate or test compounds, that bind to GAVE3 proteins  
XX or have a stimulatory or inhibitory effect on GAVE3 expression or  
XX activity. The nucleotide sequences can also be used for chromosomal  
XX mapping, tissue typing or forensic biology. Host cells comprising GAVE3  
XX can be used for producing non-human transgenic animals for studying the  
XX function and/or activity of GAVE3, or for identifying and/or evaluating  
XX modulators of GAVE3 activity  
XX  
XX Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 1038; DB 7; Length 1041;  
XX Best Local Similarity 100.0%; Pred. No. 5e-287;  
XX Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 ATGTACAAACGGTCTGCTGCGCATCGAGGGGACACCATCTCCAGGGTGAATCCCGCG 60  
XX  
XX

Db 1 ATGTACAAAGGCTGCTGTCGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Qy 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Db 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Qy 121 TGCTTCCATCAAGAGCTCGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180  
Db 121 TGCTTCCATCAAGAGCTCGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180  
Qy 181 GATTTCTCTCTTATGATCTGCTGCTTTCGGACAGACTATTAACCTCAGAGGTAGACAC 240  
Db 181 GATTTCTCTCTTATGATCTGCTGCTTTCGGACAGACTATTAACCTCAGAGGTAGACAC 240  
Qy 241 TGGGCTTTTGGGGACATTCCTTGGCGAGTGGGCTCTTTCAGCTGGCCATGAACAGGCC 300  
Db 241 TGGGCTTTTGGGGACATTCCTTGGCGAGTGGGCTCTTTCAGCTGGCCATGAACAGGCC 300  
Qy 301 GGGAGCATCGTGTCTTACGCTGGTGGCTGGGACAGGTATTTCAAAGTGGTCCACCCC 360  
Db 301 GGGAGCATCGTGTCTTACGCTGGTGGCTGGGACAGGTATTTCAAAGTGGTCCACCCC 360  
Qy 361 CACCAAGGCTGAACATCTATCTCAACCGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 420  
Db 361 CACCAAGGCTGAACATCTATCTCAACCGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 420  
Qy 421 GCCCTGGTCTCTCTGGGACAGTGTATCTTTTGTCTGGAGAACCATCTCTGGGTGCAAG 480  
Db 421 GCCCTGGTCTCTCTGGGACAGTGTATCTTTTGTCTGGAGAACCATCTCTGGGTGCAAG 480  
Qy 481 ACGGCGCTCTCTGTGAGAGCTTTCATCATGGAGTGGCCCAATGGCTGGCATGACATCAT 540  
Db 481 ACGGCGCTCTCTGTGAGAGCTTTCATCATGGAGTGGCCCAATGGCTGGCATGACATCAT 540  
Qy 541 TTCCAGCTGGAGTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 TTCCAGCTGGAGTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 601 TGGAGCTTGGGCGGAGGAGCAGCTGCTGAGCAGAGCTGCTGATGAAGAGCGGCGCG 660  
Db 601 TGGAGCTTGGGCGGAGGAGCAGCTGCTGAGCAGAGCTGCTGATGAAGAGCGGCGCG 660  
Qy 661 TTCAATCATGCTGGTGGCAATTTGTTTCATCATGCTACCTGCTGCTGCTGCTGCTGCT 720  
Db 661 TTCAATCATGCTGGTGGCAATTTGTTTCATCATGCTACCTGCTGCTGCTGCTGCTGCT 720  
Qy 721 CTCTATTTCTCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 CTCTATTTCTCTGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Qy 781 CACATACCTCTACCTTACCTACATGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 781 CACATACCTCTACCTTACCTACATGAACAGCATGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 841 TCAAGCCCTCTCTTCCCAATTTCTACCAAGCTCCTCAAAATCTGAGTGTGAACCCCAAG 900  
Db 841 TCAAGCCCTCTCTTCCCAATTTCTACCAAGCTCCTCAAAATCTGAGTGTGAACCCCAAG 900  
Qy 901 CAGCAGGACACTCAAAACACAAAGGCGGAGAGATGCCAATTTGCAACCTCGGTGCG 960  
Db 901 CAGCAGGACACTCAAAACACAAAGGCGGAGAGATGCCAATTTGCAACCTCGGTGCG 960  
Qy 961 AGGAGTGGCATCACTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020  
Db 961 AGGAGTGGCATCACTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020  
Qy 1021 CACATTGTTGAGTGGCAC 1038  
Db 1021 CACATTGTTGAGTGGCAC 1038

RESULT 11  
ABZ57957

ID ABZ57957 standard; cDNA; 1041 BP.  
XX ABZ57957;  
AC ABZ57957;  
XX 14-APR-2003 (first entry)  
DT Human respiratory chemokine receptor coding sequence.  
XX DE G-protein coupled receptor; GPCR; receptor; chemokine; human;  
KW antiasthmatic; antiinflammatory; antitussive; vaccine; gene; ss.  
XX OS Homo sapiens.  
XX EH Key Location/Qualifiers  
FT CDS 1..1041  
FT /\*tag= a  
FT /product= "Human G-protein coupled receptor"  
XX PN WO2003002604-A2.  
XX PD 09-JAN-2003.  
XX PF 25-JUN-2002; 2002WO-EP007021.  
XX PR 26-JUN-2001; 2001US-0300944P.  
XX PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.  
XX PI Bhatia U, Jones CE, Bouhelal R, Seuwen K, Tenailon L;  
XX DR WPI; 2003-210243/20.  
DR P-PSDB; ABP58453.  
XX PT New polypeptide, useful for diagnosing or treating e.g., asthma, chronic obstructive pulmonary disease, emphysema, chronic bronchitis or acute respiratory distress syndrome.  
XX PS Claim 3; Page 42-43; 44pp; English.  
XX CC The present sequence is the coding sequence for a novel human G-protein coupled receptor (GPCR) characterised as a respiratory chemokine receptor. The receptor is expressed in respiratory tissues and tissues related to monocyte/macrophage migration/activation, airway remodeling, airway fibrosis, regulation of epithelial differentiation, regulation of mucus hypersecretion, regulation of mucociliary clearance, regulation of inflammation, modulation of neutrophil, T-cell and eosinophil migration and/or activation, and regulation of epithelial cell or mast cell activation. GPCR polypeptides and polynucleotides of the invention may be useful in treatment of asthma, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, acute respiratory distress syndrome, cough and acute bronchitis. Methods of identifying agonist and antagonist compounds that stimulate or inhibit the function or level of the novel receptor are also provided. GPCR polynucleotides can also be used for recombinant production of GPCR polypeptides, as diagnostic reagents, for chromosome localisation studies, and as vaccines  
XX Qy 1 ATGTACAAAGGCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Db 1 ATGTACAAAGGCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Qy 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Db 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Qy 121 TGCTTCCATCAAGAGCTCGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180

Query Match 100.0%; Score 1038; DB 7; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTACAAAGGCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Db 1 ATGTACAAAGGCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Qy 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Db 61 CTGCTCATGTGGCTCTTGTGCTGGCGCACCTAGCAATGGGCTGCCCTGTGTGTTTC 120  
Qy 121 TGCTTCCATCAAGAGCTCGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180

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Db 121 TCGTTCACATGAAGACCTCGAAGCCAGCAGCTGTTTACCTCTTTCAATTTGGCGTGGCT 180
Qy 181 GATTTCCTCTTATGATCTGCTGCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
Db 181 GATTTCCTCTTATGATCTGCTGCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
Qy 241 TGGGCTTTTGGGACATTCCTGCGAGTGGGGCTCTTCAGTTGGGCATGAACAGGGCC 300
Db 241 TGGGCTTTTGGGACATTCCTGCGAGTGGGGCTCTTCAGTTGGGCATGAACAGGGCC 300
Qy 301 GGGAGCATCGTGTTCCTTAAGTGGTGGTGGCGACAGGTATTATTTCAAGTGGTCCACCC 360
Db 301 GGGAGCATCGTGTTCCTTAAGTGGTGGTGGCGACAGGTATTATTTCAAGTGGTCCACCC 360
Qy 361 CACCACCGGTGAACACTATCTCCACCCGGGTGGCGCTGSCATCGTCTGCACCTCTGG 420
Db 361 CACCACCGGTGAACACTATCTCCACCCGGGTGGCGCTGSCATCGTCTGCACCTCTGG 420
Qy 421 GCCTGTGTCATCTCGGAACAGTGTATCTTTTGTCTGGAGAACCATCTCTGCGTGCAGAG 480
Db 421 GCCTGTGTCATCTCGGAACAGTGTATCTTTTGTCTGGAGAACCATCTCTGCGTGCAGAG 480
Qy 481 ACGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCCAATGGCTGGCATGACATCATG 540
Db 481 ACGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCCAATGGCTGGCATGACATCATG 540
Qy 541 TTCAGCTGAGTGTCTTTATGCCCTCGGCATCATCTTATTTTCTCTTCAAGATTGTT 600
Db 541 TTCAGCTGAGTGTCTTTATGCCCTCGGCATCATCTTATTTTCTCTTCAAGATTGTT 600
Qy 601 TGGAGCTGAGGGGAGGAGAGCTGCGCCAGACAGCTCGGATGAAGAGGCGACCCGG 660
Db 601 TGGAGCTGAGGGGAGGAGAGCTGCGCCAGACAGCTCGGATGAAGAGGCGACCCGG 660
Qy 661 TTCTATCATGCTGTGGCAATGTGTTTCATCATGCTACCTGCGCAGCGTGTCTGTAGA 720
Db 661 TTCTATCATGCTGTGGCAATGTGTTTCATCATGCTACCTGCGCAGCGTGTCTGTAGA 720
Qy 721 CTCTATTTCTCTGGAGCGTCCCTCGAGTGGCTGCGATCCCTCTGTCATGGGGCCCTG 780
Db 721 CTCTATTTCTCTGGAGCGTCCCTCGAGTGGCTGCGATCCCTCTGTCATGGGGCCCTG 780
Qy 781 CACATTAACCTCGATTCTACATGAACAGCATGCTGGATCCCTGCTGTATTTATTTT 840
Db 781 CACATTAACCTCGATTCTACATGAACAGCATGCTGGATCCCTGCTGTATTTATTTT 840
Qy 841 TCAAGCCCTCTCTTCCAAATTTCTACACAGCTCAAAATCTGAGTCTGAAACCCAG 900
Db 841 TCAAGCCCTCTCTTCCAAATTTCTACACAGCTCAAAATCTGAGTCTGAAACCCAG 900
Qy 901 CAGCCAGGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTTGAACCTCGGTCC 960
Db 901 CAGCCAGGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTTGAACCTCGGTCC 960
Qy 961 AGAGTGTGATCATGTGTGCAATAGTTTCAAGCCAGTCTGATGGGCAATGGATCCC 1020
Db 961 AGAGTGTGATCATGTGTGCAATAGTTTCAAGCCAGTCTGATGGGCAATGGATCCC 1020
Qy 1021 CACATTTGTTGAGTGGCAC 1038
Db 1021 CACATTTGTTGAGTGGCAC 1038
```

RESULT 12

AAD61654

ID AAD61654 standard; DNA, 1041 BP.

XX

AC AAD61654;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human GPCRxl4 DNA.

XX

Human; G-protein coupled receptor; GPCR; infection; neoplastic process; inflammation; myocardial infarction; atherosclerosis; angina pectoris; hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain; diabetes; cancer; virucide; analgesic; cardiant; gene; ds.

Homo sapiens.

Key Location/Qualifiers  
CDS 1..1041  
/\*tag= a  
/product= "Human GPCR protein"

US2003108986-A1.

12-JUN-2003.

20-FEB-2002; 2002US-00079384.

21-JUN-2001; 2001US-00885453.

(EURO-) EUROSREEN SA.

Communi D, Lannoy V, Brezillon S, Dethoux M, Parmentier M;  
Govaerts C;

WPI: 2003-810852/76.

P-PSDB; ABW00810.

Novel G-protein coupled receptor useful for treating viral infections, bacterial infections, fungal infections, cancer, diabetes, hypertension, osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.

Claim 5; Fig 9; Opp; English.

The present invention relates to novel G-protein coupled receptors (GPCRs) and the nucleic acids encoding them. The invention is useful for treating viral, bacterial and fungal infections, inflammatory and neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer, angina pectoris, myocardial infarction and atherosclerosis. The present sequence is human G-protein coupled receptor (GPCR) DNA

Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 9; Length 1041;

Best Local Similarity 100.0%; Pred. No. 5e-287;

Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60

Db 1 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60

Qy 61 CTGCTCAATCTGCGCTTTGTCTGGGCGCACTAGGCGGCTGCGCTGCTGCTGCTTC 120

Db 61 CTGCTCAATCTGCGCTTTGTCTGGGCGCACTAGGCGGCTGCGCTGCTGCTGCTTC 120

Qy 121 TCGTTCACATGAAGACCTCGAAGCCAGACACTGTTTACCTTTTCAATTTGGCGTGGCT 180

Db 121 TCGTTCACATGAAGACCTCGAAGCCAGACACTGTTTACCTTTTCAATTTGGCGTGGCT 180

Qy 181 GATTTCCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Db 181 GATTTCCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Qy 241 TGGGCTTTTGGGACATTCCTGCGAGTGGGGCTCTTACGTTGGGCATGAACAGGGCC 300

Db 241 TGGGCTTTTGGGACATTCCTGCGAGTGGGGCTCTTACGTTGGGCATGAACAGGGCC 300

Qy 301 GGGAGCATCGTGTTCCTTACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360

Db 301 GGGAGCATCGTGTTCCTTACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360

Qy 361 CACCACCGGTGAACACTATCTCCACCCGGGTGGCGCTGSCATCGTCTGCACCTCTGG 420

Db 361 CACCACCGGTGAACACTATCTCCACCCGGGTGGCGCTGSCATCGTCTGCACCTCTGG 420

```
Db 361 CACCACGGGTGAACATATCTCCACCCGGGTGGGGCTGGCATCGTCTGCACCCCTGTGG 420
Qy 421 GCCTGGTCACTCTGGGAACAGTGTATCTTTTGTGAGAGAACCATCTCTCTGGTGCAGAG 480
Db 421 GCCTGGTCACTCTGGGAACAGTGTATCTTTTGTGAGAGAACCATCTCTCTGGTGCAGAG 480
Qy 481 ACCGCCCTCTCTGTGAGAGCTTCATCATGAGTGGCCCAATGCTGGCATGACATCATG 540
Db 481 ACCGCCCTCTCTGTGAGAGCTTCATCATGAGTGGCCCAATGCTGGCATGACATCATG 540
Qy 541 TTCAGCTGAGTCTTTATAGCCCTCGGCATCATCTTTATTTTCTCTCTCAAGATGTT 600
Db 541 TTCAGCTGAGTCTTTATAGCCCTCGGCATCATCTTTATTTTCTCTCTCAAGATGTT 600
Qy 601 TGGAGCTGAGCGGCGGAGCGAGCTGGCCAGACAGGCTGGATGAGAGAGGCGACCCGG 660
Db 601 TGGAGCTGAGCGGCGGAGCGAGCTGGCCAGACAGGCTGGATGAGAGAGGCGACCCGG 660
Qy 661 TTCATCATGCTGGTGGCAATTTGTCTTCATCATGCTACCTGCCAGCGTGTCTGTAGA 720
Db 661 TTCATCATGCTGGTGGCAATTTGTCTTCATCATGCTACCTGCCAGCGTGTCTGTAGA 720
Qy 721 CTCTATTTCTCTGGAAGGTCCTCGAGTGGCCCTGAGTGGCCGATCCCTCTGTCCATGGGCGCTG 780
Db 721 CTCTATTTCTCTGGAAGGTCCTCGAGTGGCCCTGAGTGGCCGATCCCTCTGTCCATGGGCGCTG 780
Qy 781 CACATACCTCTCAGCTTCACCTACATCATGACAGCATGCTGGATCCCTGCTGTTATTTT 840
Db 781 CACATACCTCTCAGCTTCACCTACATCATGACAGCATGCTGGATCCCTGCTGTTATTTT 840
Qy 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCCAAG 900
Db 841 TCAAGCCCTCTCTTCCCAATTTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCCAAG 900
Qy 901 CAGCCAGGACACTCAAAAACACAAAGCGCGGAGAGATGCCAATTTGAACTCTGGTGGC 960
Db 901 CAGCCAGGACACTCAAAAACACAAAGCGCGGAGAGATGCCAATTTGAACTCTGGTGGC 960
Qy 961 AGAGGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020
Db 961 AGAGGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020
Qy 1021 CACATTTGTTGAGTGGCAC 1038
Db 1021 CACATTTGTTGAGTGGCAC 1038

RESULT 13
ABAB1530
ID ABAB1530 standard; DNA; 1050 BP.
XX
AC ABAB1530;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human GPCR1b polynucleotide SEQ ID NO 3.
XX
KW Human; GPCR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
KW anabolic; cytosclastic; antiviral; gene therapy; cardiomyopathy; obesity;
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW infection; human immunodeficiency virus; HIV; ds.
XX
OS Homo sapiens.
XX
XX WC020174904-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US010241.
XX
PR 31-MAR-2000; 2000US-0193664P.
PR 05-APR-2000; 2000US-0194614P.
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PR 06-APR-2000; 2000US-0195063P.
PR 06-APR-2000; 2000US-0195066P.
PR 06-APR-2000; 2000US-0195067P.
PR 06-APR-2000; 2000US-0195068P.
PR 06-APR-2000; 2000US-0195069P.
PR 06-APR-2000; 2000US-0195070P.
PR 06-APR-2000; 2000US-0195101P.
PR 21-JUL-2000; 2000US-0219855P.
PR 27-JUL-2000; 2000US-0221284P.
PR 28-JUL-2000; 2000US-0221325P.
PR 11-AUG-2000; 2000US-0224588P.
PR 11-OCT-2000; 2000US-0239613P.
PR 18-JAN-2001; 2001US-0262508P.
PR 23-JAN-2001; 2001US-0263433P.
PR 23-JAN-2001; 2001US-0263604P.
PR 30-JAN-2001; 2001US-0265161P.
PR 29-MAR-2001; 2001US-00823172.
XX
(CURA-) CURAGEN CORP.
PA
XX Majumder X, Vercet CM, Casman SJ, Wolenc AR, Spaderna SK;
XX Padigaru M, Mishnu VS, Tchernev VT, Spytek KA, Li L, Baumgartner JC;
XX Gusev VY;
XX WPI; 2001-639351/73.
XX P-PSDB; ABB44522.
XX
XX New human G-protein coupled receptor X, GPCRX, polypeptide useful in
XX treatment or prevention of GPCR associated disorders e.g. cardiomyopathy
XX or atherosclerosis, and to screen for antagonists and agonists useful
XX therapeutically.
XX
XX Claim 9; Page 10; 157pp; English.
XX
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
XX encode G-coupled protein-receptor related polypeptides (ABB44522-
XX ABB44543). The isolated polypeptide having a sequence differing by no
XX more than 15 % of amino acid residues from one of 22 amino acid sequences
XX (or mature forms of the sequences), fully defined in the specification
XX and corresponding to human G-protein coupled receptor X (GPCRX)
XX polypeptides. The polypeptides have potential cardiant,
XX antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
XX polypeptides can be administered therapeutically, especially using gene
XX therapy and expressing the encoding DNA in vivo, to treat or prevent
XX GPCR-associated disorders, especially in humans. For example, they can
XX be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
XX related to signal processing and metabolic pathway modulation (e.g.
XX obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
XX sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
XX disease, Parkinson's disorder, Huntington's disease), immune disorders,
XX haematopoietic disorders, developmental diseases, neurological disorders,
XX bacterial, fungal, protozoal and viral infections (e.g. with human
XX immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
XX to determine the presence of or predisposition to a disease associated
XX with altered levels of the polypeptide in mammals (especially humans) by
XX detecting alterations in polypeptide expression levels relative to
XX control samples. They are useful to identify agents binding polypeptide
XX (e.g. cellular receptors or downstream effectors) and/or agents
XX modulating cellular polypeptide expression or activity, useful as
XX antagonists and agonists in disease treatment
XX
XX Sequence 1050 BP; 211 A; 298 C; 279 G; 262 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 1038; DB 4; Length 1050;
Best Local Similarity 100.0%; Pred. No. 5e-287;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60
Db 6 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 65
Qy 61 CTGCTCATTTGGCTTTGTGCTGGCGCATAGGCAATGGGTCGCCCTGTGGTTTC 120
```



Db 66 CTGCTCATTTGGCCTTTGTGCTGGCGGCACCTAGGCAATGGGTCGCCCTGTGTGGTTTC 125  
Qy 121 TGCCTCCACATGAACACCTGGAGCCAGCAGCTGTTTACCTTTTCAATTTGGCCTGGCT 180  
Db 126 TGCCTCCACATGAACACCTGGAGCCAGCAGCTGTTTACCTTTTCAATTTGGCCTGGCT 185  
Qy 181 GATTTTCCTCTTATCATCTGCTGCTGCTTTTCGACAGACTATTACTCTCAGAGCTAGACAC 240  
Db 186 GATTTTCCTCTTATCATCTGCTGCTGCTTTTCGACAGACTATTACTCTCAGAGCTAGACAC 245  
Qy 241 TGGGCTTTTGGGGAATTCCTCCGCGAGTGGGGCTTTCACGTTGGCCCATGAACAGGGCC 300  
Db 246 TGGGCTTTTGGGGAATTCCTCCGCGAGTGGGGCTTTCACGTTGGCCCATGAACAGGGCC 305  
Qy 301 GGGAGCATCGTTCCTTACCGTGGTGGCTGGGACAGGTATTTCAAGTGGTCCACCC 360  
Db 306 GGGAGCATCGTTCCTTACCGTGGTGGCTGGGACAGGTATTTCAAGTGGTCCACCC 365  
Qy 361 CACCAAGCGGTGAACACTATCTCCACCGGGTGGCGCTGGCATCGTCTGCACCCCTGTGG 420  
Db 366 CACCAAGCGGTGAACACTATCTCCACCGGGTGGCGCTGGCATCGTCTGCACCCCTGTGG 425  
Qy 421 GCCCTGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACATCTCTGGCTGCAAGAG 480  
Db 426 GCCCTGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACATCTCTGGCTGCAAGAG 485  
Qy 481 ACGGCGGTCTCTGTGAGAGCTTCATCATGAGTGGCCAAATGGCTGGCATCACATCATG 540  
Db 486 ACGGCGGTCTCTGTGAGAGCTTCATCATGAGTGGCCAAATGGCTGGCATCACATCATG 545  
Qy 541 TTCAGCTGGAGTTCTTTATGCCCTCGGCATCATCTTTATTTTGTCTCTTCAAGATTGTT 600  
Db 546 TTCAGCTGGAGTTCTTTATGCCCTCGGCATCATCTTTATTTTGTCTCTTCAAGATTGTT 605  
Qy 601 TGGAGCTGAGCGGAGCGACGATGCGCCACAGGCTGGATGAGAGAGGACCGCG 660  
Db 606 TGGAGCTGAGCGGAGCGACGATGCGCCACAGGCTGGATGAGAGAGGACCGCG 665  
Qy 661 TTCATCATGTTGGTGGCAATTTGTTTCATCATGCTACCTGCCAGCGTGTCTGTCTAGA 720  
Db 666 TTCATCATGTTGGTGGCAATTTGTTTCATCATGCTACCTGCCAGCGTGTCTGTCTAGA 725  
Qy 721 CTCTATTTCTCTGACGGTGGCTCGAGTGGCTCGATGCCCTCTGTCTCATGGGCGCTCG 780  
Db 726 CTCTATTTCTCTGACGGTGGCTCGAGTGGCTCGATGCCCTCTGTCTCATGGGCGCTCG 785  
Qy 781 CACATAACCCCTCAGCTTCACCTACATGACGATGCTGGATCCCTGCTGTATTATTATT 840  
Db 786 CACATAACCCCTCAGCTTCACCTACATGACGATGCTGGATCCCTGCTGTATTATTATT 845  
Qy 841 TCAAGCCCTCTCTTTCCCAAAATTTACAAACAGCTCAAAATCTGCAGTCTGAAACCCAG 900  
Db 846 TCAAGCCCTCTCTTTCCCAAAATTTACAAACAGCTCAAAATCTGCAGTCTGAAACCCAG 905  
Qy 901 CAGCCAGACACTCAAAACACAAAGCGCGGAGAGATGCCAAATTCGAACCTCGGTGCG 960  
Db 906 CAGCCAGACACTCAAAACACAAAGCGCGGAGAGATGCCAAATTCGAACCTCGGTGCG 965  
Qy 961 AGGAGTGCATCAGTGTGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020  
Db 966 AGGAGTGCATCAGTGTGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1025  
Qy 1021 CACATTGTTAGTGGCAC 1038  
Db 1026 CACATTGTTAGTGGCAC 1043

RESULT 14  
ID ABA81529  
XX ABA81529 standard; DNA; 1050 BP.  
AC ABA81529;  
XX

DT 28-JAN-2002 (first entry)  
XX Human GPCR1a polynucleotide SEQ ID NO 1.  
DE Human; GPCR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;  
XX anabolic; cytotatic; antiviral; gene therapy; cardiomyopathy; obesity;  
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;  
KW asthma; Alzheimer's disease; Parkinson's disease; Huntington's disease;  
KW infection; human immunodeficiency virus; HIV; ds.  
XX Homo sapiens.  
OS WC200174904-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US010241.  
XX 31-MAR-2000; 2000US-0193664P.  
PR 05-APR-2000; 2000US-0194614P.  
PR 06-APR-2000; 2000US-0195063P.  
PR 06-APR-2000; 2000US-0195066P.  
PR 06-APR-2000; 2000US-0195067P.  
PR 06-APR-2000; 2000US-0195068P.  
PR 06-APR-2000; 2000US-0195069P.  
PR 06-APR-2000; 2000US-0195070P.  
PR 21-JUL-2000; 2000US-0195510P.  
PR 21-JUL-2000; 2000US-02119855P.  
PR 27-JUL-2000; 2000US-0221284P.  
PR 28-JUL-2000; 2000US-0221325P.  
PR 11-AUG-2000; 2000US-0224588P.  
PR 11-OCT-2000; 2000US-0239613P.  
PR 18-JAN-2001; 2001US-0262508P.  
PR 23-JAN-2001; 2001US-0263433P.  
PR 23-JAN-2001; 2001US-0263604P.  
PR 30-JAN-2001; 2001US-0265161P.  
PR 29-MAR-2001; 2001US-00823172.  
XX (CURA-) CURAGEN CORP.  
XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;  
PI Padigaru M, Mishnu VS, Tchernev VI, Spytek KA, Li L, Baumgartner JC;  
PI Gusev VI;  
XX WPI: 2001-639351/73.  
XX P-PSDB; ABB44522.  
DR New human G-protein coupled receptor X, GPCR, polypeptide useful in  
XX treatment or prevention of GPCR associated disorders e.g. cardiomyopathy  
PT or atherosclerosis, and to screen for antagonists and agonists useful  
PT therapeutically.  
XX Claim 9; Page 7; 157pp; English.  
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that  
CC encode G-coupled protein-receptor related polypeptides (ABA44522-  
CC ABB44543). The isolated polypeptide having a sequence differing by no  
CC more than 15 % of amino acid residues from one of 22 amino acid sequences  
CC (or mature forms of the sequences), fully defined in the specification  
CC and corresponding to human G-protein coupled receptor X (GPCRX)  
CC polypeptides. The polypeptides have potential cardiant,  
CC antiarteriosclerotic, anabolic, cytotatic and antiviral activity. The  
CC polypeptides can be administered therapeutically, especially using gene  
CC therapy and expressing the encoding DNA in vivo, to treat or prevent  
CC GPCR-associated disorders, especially in humans. For example, they can  
CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders  
CC related to signal processing and metabolic pathway modulation (e.g.  
CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple  
CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease), immune disorders,  
CC hematopoietic disorders, developmental diseases, neurological disorders,  
CC bacterial, fungal, protozoal and viral infections (e.g. with human  
CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically

CC to determine the presence of or predisposition to a disease associated  
CC with altered levels of the polypeptide in mammals (especially humans) by  
CC detecting alterations in polypeptide expression levels relative to  
CC control samples. They are useful to identify agents binding polypeptide  
CC (e.g. cellular receptors or downstream effectors) and/or agents  
CC modulating cellular polypeptide expression or activity, useful as  
CC antagonists and agonists in disease treatment

XX SQ Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 4; Length 1050;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTGCTCAATTTGGCCCTTTGTCGTCGGCGCACTAGGCAATGGGCTGCGCCCTGTGTGTTTC 125
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DB 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGGCTTTCACTTGGCCATGAACAGGGCC 305
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QY 361 CACACGCGGTGAACACATCTTCCACCGGGTGGGGCTGGCATCTGTCGACCCCTGTGG 420
DB 361 CACACGCGGTGAACACATCTTCCACCGGGTGGGGCTGGCATCTGTCGACCCCTGTGG 425
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DB 421 GCGCTGCTATCTCTGGGACAGTGTATCTTTGCTGGAGAACCATCTCTGCTGCAAGAG 485
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QY 541 TCCAGCTGGAGTCTTTATGCGCCCTCGGSCATCATCTTTATTTGCTTCAAGATTGTT 600
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QY 781 CACATACCTCTCAGCTTCACTTACATGAACAGCATGCTGATCCCTGCTGATTTATTT 840
DB 781 CACATACCTCTCAGCTTCACTTACATGAACAGCATGCTGATCCCTGCTGATTTATTT 845
QY 841 TCAAGCGCTCTCTTCCAAATTTTACAAAGCTCAAAATCTGAGTCTGAACCCCAAG 900
DB 841 TCAAGCGCTCTCTTCCAAATTTTACAAAGCTCAAAATCTGAGTCTGAACCCCAAG 905
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QY 901 CAGCCAGGACACTCAAAAACACAAAGGCGGAGAGATGCCAATTTGGAACCTCGGTGCG 960
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QY 961 AGGAGTTGTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
DB 966 AGGAGTTGTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1025
QY 1021 CACATTGTTGAGTGGCAC 1038
DB 1026 CACATTGTTGAGTGGCAC 1043
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## RESULT 15

ADE40271

ID ADE40271 standard; cDNA; 1050 BP.

XX AC ADE40271;

XX AC ADE40271;

DT 29-JAN-2004 (first entry)

XX Human NOV41a cDNA - SEQ ID 177.

DE Human NOV41a cDNA - SEQ ID 177.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;

XX antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;

XX antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;

XX atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

XX multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;

XX asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;

XX tissue typing; human; NOV; ss; gene.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003064589-A2.

XX PD 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

XX 17-AUG-2001; 2001US-0313201P.

XX 20-AUG-2001; 2001US-0313643P.

XX 21-AUG-2001; 2001US-0313702P.

XX 23-AUG-2001; 2001US-0314466P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 17-SEP-2001; 2001US-0322716P.

XX 21-SEP-2001; 2001US-0323994P.

XX 14-DEC-2001; 2001US-0340233P.

XX 05-FEB-2002; 2002US-0354591P.

XX 19-MAR-2002; 2002US-0365478P.

XX 19-APR-2002; 2002US-0373814P.

XX 19-APR-2002; 2002US-0373825P.

XX 19-APR-2002; 2002US-0373989P.

XX 23-APR-2002; 2002US-0374632P.

XX 01-JUN-2002; 2002US-0386971P.

XX 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;

XX Shinketsu RM, Zernhusen BD, Li L, Ji W, Padigaru M, Casman SJ;

XX Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;

XX Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;

PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;  
PI Alsebrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR,  
PI Smithson G;  
XX WPI: 2003-663472/62.  
DR P-PSDB: ADE40272.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX Claim 20; SEQ ID NO 177; 560pp; English.  
XX  
XX The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,  
CC cytotatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, neotropic, antiparkinsonian, antiasthmatic and  
CC gynaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the human NOVX cDNA of the invention.  
XX  
SQ Sequence 1050 BP; 211 A; 298 C; 279 G; 262 T; 0 U; 0 Other;

Query Match 100.0%; Score 1038; DB 9; Length 1050;  
Best Local Similarity 100.0%; Pred. No. 5e-287;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTCGTGCTGCCCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60  
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QY 966 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1025  
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Db  
QY 1026 CACATTTGTTGAGTGGCAC 1043

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Job time : 523 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfileseq.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	367.6	35.4	2051	4	US-09-023-655-1212
4	366	35.3	1164	4	US-09-170-496D-221
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6	229.6	22.1	545	2	US-08-771-182-1
7	229.6	22.1	545	3	US-08-853-194-1
8	188.8	18.2	1594	2	US-08-955-713-1
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12	137.6	13.3	960	4	US-09-170-496D-195
13	136	13.1	960	4	US-09-170-496D-59
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16	109	10.5	1901	1	US-08-153-848-43
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45	75.8	7.3	1255	1	US-08-097-938-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-170-496D-107

; Sequence 107, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 234

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 107

; LENGTH: 1164

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-170-496D-107

Query Match	35.4%	Score 367.6;	DB 4;	Length 1164;
Best Local Similarity	63.9%	Pred. No. 1e-96;		
Matches 597;	Conservative	0;	Mismatches 319;	Indels 18;
Gaps	2;			
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Qy	301	GGGAGCATCGTGTTCCTTACGGTGTGTGCTTCGGACAGGTATTTCAAAGTGTCCACCC	360	
Db	337	GGCAGCATCATCTTCTCCTCAGCGTGTGTGCGGTAGACAGGTATTTCCGGGTGTCTCCATCC	396	
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Db 457 GGCATCACTGTTGGCCCTTAACAGTCCACCTCTGAAGAAGATTGCTGATCCAGAAATGGC 516
Qy 481 ACCGCCGTCTCTGTGAGAGCTTCATCATGAGTCCGCCAAATGGCTGGCATGACATCATG 540
Db 517 CTGCAAAATGTGTGATCAGCTTCAGCATCTGCCATACCTTCGGTGGCAGAGCTATG 576
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Db 754 ATCCGATCTCTCTGTGGCAATTTGTTTATCATCATGCTTACCTGCCCCAGCTGTCTGTG 813
Qy 766 GTCCATGAGGCGCTGACATAAACCCTCAGCTTACCTGATGAGAGGCGACCCG 825
Db 814 GTGAGCTGCGGCTTTTATCATCTCAGCTTACCTGATGAGAGGCGACCCG 873
Qy 826 CTGCTGATTTATTTTCAAGCCCTCTCTTTCCAAATTTCAACAAAGCTCAAAATCTGC 885
Db 874 GTGCTGATTTATTTTCAAGCCCTCTCTTTCCAAATTTCAACAAAGCTCAAAATCTGC 933
Qy 886 AGTCTGAAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 919
Db 934 TGCCCTCAGGAAGATGACAGGTCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 967
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## RESULT 2

```
US-09-016-434-1259
; Sequence 1259, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
```

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; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2051 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G219866
; US-09-016-434-1259
```

```
Query Match 35.4%; Score 367.6; DB 4; Length 2051;
Best local similarity 63.9%; Pred. No. 1.3e-96;
Matches 597; Conservative 0; Mismatches 319; Indels 18; Gaps 2;

Qy 1 ATGTACAAAGGCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60
Db 97 ATAGACAGAGAACTGCTGTGTGTTCCGAGATGACTTCAATGCCAAGGTGTTGCGCGG 156
Qy 61 CTGCTCATGTTGGCTTTGCTGTGGGCGCATAGGCAATGGGGTGGCCCTGTGTGTTTC 120
Db 157 GTGTTGGGGCTGAGATTATCTTTGGGCTTCTGGGCAATGGCCCTTGGCCCTGTGATTTTC 216
Qy 121 TGCTTCCATGATGAGACTCGAAGCCAGACACTGTTTACCTTTTCAATTTGGCCGTGCT 180
Db 217 TGTTTCCACTCAAGTCTCGAAATCCAGCGGATTTTCTGTTCATCTGGCAGTAGCT 276
Qy 181 GATTTCCTCTTATGATCTGCTGCTTTCGGACAGACTATTTACCTCAGACGTAGACAC 240
Db 277 GACTTCTACTGATCATCTGCTGCGCTTCGTGATGACTACTATGTGCGCGTTTCAGAC 336
Qy 241 TGGCTTTTGGGACATTCCTGCGGAGTGGGGCTTTCAGTTGGGCTATGAAAGGGCC 300
Db 337 TGGAACTTTGGGACATCCCTTGGCGGCTGCTGCTTCTCATGTTTGGCATGAACGCCAG 396
Qy 301 GGGAGCATCTGTTTCTTACGCTGCTGCGGACAGGATTTTCAAGTGTCCACCC 360
Db 397 GGCAGCATCATCTTCTCAGGTTGGCGGTGACAGGATTTTCCGGGTGTTCCATCCC 456
Qy 361 CACCACGCGTGAACACTATCTCCACCGGCTGGCGGTGCGCATCTGTCGACCCCTGTGG 420
Db 457 CACCACGCTGAACAGATCTCCAAATTGGACAGCAGCCATCATCTCTGCTTCTGTGG 516
Qy 421 GCCTGTGATCTGCGGACAGTATCTTTTGTGAGAACCATCTCTGCTGGTGAAGAG 480
Db 517 GGCATCATCTGTTGGCTTAAACAGTCCACCTCTGAAGAAGATTGCTGATCCAGATGGC 576
Qy 481 ACGCCCTCTCTGTGAGAGCTTCATCATGAGTCCGCCCAATGGCTGGCATGACATCATG 540
Db 577 CTGCAAAATGTGTGATCAGCTTCAGCATCTGCCATACCTTCGGTGGCAGAGCTATG 636
Qy 541 TTCAGCTGAGTCTTTATGCCCCCTGGCATCATCTTTATTTGCTCTCTTCAAGATTGTT 600
Db 637 TTCTCTCTGAGTCTCTCTGCCCCCTGGGCATCATCTCTGCTTCTGCTCAGCCAGAAATTATC 696
Qy 601 TGGAGCTGAGGCGGAGCAGCTGGCCAGACAGCTCGGATGAGAGGCGACCCG 660
Db 697 TGGAGCTGCGGAGAG---ACAAATGAGCGGATGCCAAGATCAAGAGAGCCATCACC 753
Qy 661 TTCTATGCTGTGGCAATTTGTTTATCATCATGCTTACCTGCCCCAGCTGTCTGTGAGA 720
Db 754 TTCTATGCTGTGGCAATTTGTTTATCATCATGCTTCTGCTTCTGCTCAGCCAGTGTGTTG 813
Qy 721 CTCTATTTCTCTGTGGAGTGGCCCTC-----GAGTGGCTGCGATCCCTCT 765
Db 814 ATCCGATCTCTCTGTGGCAATTTGTTTATCATCATGCTTCCGGCAGCAGAAATTTGTAAGTGTACCGCTCG 873
Qy 766 GTCCATGAGGCGCTGACATAAACCCTCAGCTTACCTGATGAGAGGCGACCCG 825
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Db 874 GTGACCTGGCGTTCTTTATCACTCTCAGCTTCACTACATGAACAGCATGCTGGACCCC 933  
Qy 826 CTGGCTATATATTTTCAAGCCCTCTTTCCAAATTTCTACACAGCTCAAAATCTGC 885  
Db 934 GTGGTGTAATACTTCTCCAGCCCATCTTTCCCAACTTCTTCCCACTTTGATCAACCCG 993  
Qy 886 AGTCTGAACCCCAAGCAGCCAGGACACTCAAAA 919  
Db 994 TGCCTCCAGAGGAGATGACAGGTGAGCCAGATA 1027

## RESULT 3

US-09-023-655-1212  
; Sequence 1212, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DCS 6.2  
; CURRENT APPLICATION DATA:  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1212:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2051 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g219866  
; US-09-023-655-1212

Query Match 35.4%; Score 367.6; DB 4; Length 2051;  
Best Local Similarity 63.9%; Pred. No. 1.3e-96;  
Matches 597; Conservative 0; Mismatches 319; Indels 18; Gaps 2;  
Qy 1 ATGTACAAAGGCTGCTGCTGGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGCG 60  
Db 97 ATAGACAAGAAGAACTCTGTGTTCGAGATGACATTCATTGCAAGGTGTTGCGCGCG 156  
Qy 61 CTGCTCATTTGGCTTTGTGCTGGCGCATAGGCATGGGTGCGCCCTGTGTGTTTC 120  
Db 157 GTGTGGGCTGTGGGCTTATCTTTGGGCTTCTGGGCAATGGCCCTGCGGCTGTGATTTTC 216  
Qy 121 TGCTTCCACATGAAGACCTGGAAGCCCGACGACTGTTTACCTTTTCAATTTGGCGGTGGCT 180

Db 217 TGTTTCACCTCAAGTCTCGAAATCCAGCGGATTTTCTGTTCACCTGCGAGTAGCT 276  
Qy 181 GATTTCCTCTTATGATCTGCTGCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240  
Db 277 GACTTTCTACTGATCATCTGCTGCTGCTTGTGATGAGACTACTATGTGCGGCTCAGAC 336  
Qy 241 TGGGCTTTTGGGACATTTCCCTGCGGAGTGGGGCTCTTCACTGTTGGCCATGAACAGGCGCC 300  
Db 337 TGGAACTTTGGGACATCTCTTGGCGCTGGTCTCTTCATGTTTGCATGAACCGCCAG 396  
Qy 301 GGGAGCATCTGTTCCTTACGGTGGTGGCTGCGACAGAGTATTCAAAGTGGTGCACCCC 360  
Db 397 GGCAGCATCATCTTCTCTCAGGGTGGTGGCTAGACAGGTATTTCCGGGTGGTCCATCCC 456  
Qy 361 CACACGGGTGACACTATCTCCACCGGGTGGCGGTGGCATCGTCTGCACTCTGTTGG 420  
Db 457 CACACCGCTGGAACAAGATCTCCAATTGGACAGCGCCATCATCTCTTGGCTTCTGTGG 516  
Qy 421 GCCTGTGTCATCTCTGGGACAGTGTATCTTTTGTGGAGAACCATCTCTGGGTGCAAGAG 480  
Db 517 GGCATCACTGTGGCTTAACAGTCCACTCTCTGAAGAAGAAGTTGCTGATCCAGATGCG 576  
Qy 481 ACGGCGCTCTCTGTGAGAGTTCATCATGAGGTGGGCAATGCTGGCTGGCATGACATCATG 540  
Db 577 CCGCAAAATGTGTCATCAGCTTCAGCATCTGCCATACCTTCCGGTGGCACCAAGCTATG 636  
Qy 541 TTCCAGCTGGAGTCTTTATGCCCTCGGCATCATCTTATTTTCTCTCTTCAAGATTGTT 600  
Db 637 TTCTCTCTGGAGTCTCTCTGCGCTGGGCATCACTCTGTTCTCTCAGCCAGATTAATC 696  
Qy 601 TGGAGCTGAGGGGAGGCGAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGCGGACCCGG 660  
Db 697 TGGAGCTTGGCGAGAG--ACAAATGGAACGGCATGCCAAGATCAAGAGAGCCATCAC 753  
Qy 661 TTCAATGAGTGGGCAATTTGTTTTCATCATGATGCTACCTGCGGAGGCTGCTGCTAGA 720  
Db 754 TTCAATGAGTGGGCAATGCTTGTGTCATCTGCTTCTCTCCAGCGGTGTTGTCGG 813  
Qy 721 CTCATTTCTCTGAGCGGTGCCCTC-----GAGTGCCTGGATCCCTCT 765  
Db 814 ATCCGATCTTCTGGCTCTGTCACACTTCGGGACGCGAAGATTGTGAAGTACCGTCTG 873  
Qy 766 GTCCATGGGCGCTCGACATAAACCTCAGCTTTCACCTACATGAACAGCATCTGATCCC 825  
Db 874 GTGGACCTGGGCTCTTTTATCACTCTCAGCTTTCACCTACATGAACAGCATCTGACCCC 933  
Qy 826 CTGGTGTATTTTTCAGGCGCTCTTTTCCAAATTTCTACAAAGCTCAAAATCTGC 885  
Db 934 GTGGTGTACTACTTCTCCAGCCCATCTTTCCTCCAACTTCTTCTCCACTTTGATCAACCGC 993  
Qy 886 AGTCTGAACCCCAAGCAGCCAGGACACTCAAAA 919  
Db 994 TGCCTCCAGAGGAGATGACAGGTGAGCCAGATA 1027

## RESULT 4

US-09-170-496D-221  
; Sequence 221, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 221  
; LENGTH: 1164

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-221

Query Match      35.3%; Score 366; DB 4; Length 1164;
Best Local Similarity 63.8%; Pred. No. 2.9e-96;
Matches 596; Conservative 0; Mismatches 320; Indels 18; Gaps 2;

QY 1 ATGTACACGGTCTGCTGCGCATCGAGGGGACACCACTCTCCAGGTGATGCCCGG 60
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
37 ATAGACAAGAGAACTCTCTGTGTTCCGAGATGACTTCATTCGCAAGGTGTTCGCGCG 96
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 CTGCTCATCTGGGCTTTGCTGCGGCGCACTAGGCAATGGGTCGCCCTGTGTGTTTC 120
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
97 GTGTGGGCTGGAGTTTATCTTTGGGCTTCGGGCAATGGCCCTTGCCCTGTGATTTTC 156
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 TGTTCACATGAAGACCTGGAAGCCGACGACTGTGTTTACCTTTTCAATTTGGCGNGGCT 180
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
157 TGTTCACCTCAAGTCTGGAATCCAGCGGATTTTCTGTTCACCTGGCAGTAGCT 216
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTACCTCAGACGTAGACAC 240
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 GACTTTCTACTGATCACTCTGCTGCGGCTCGTGATGACTACTATGTGCGGCGTTACAG 276
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 TGGGCTTTTGGGACATTCCTCGCGAGTGGGCTCTTTCAGTTGGCCATGAACAGGGCC 300
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
277 TGGAGTTTGGGACATCCCTTGGCGGCTGGTCTCTTCATGTTGCCATGAACCGCGAG 336
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 GGAGCATCTGTTCCTTAGCTGGTGGCTGGGACAGGATTTTCAAGTGGTCCACCC 360
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
337 GGAGCATCATCTCTTCAAGTGGTGGGCTGGGACAGGATTTTCCGGTGGTCCATCCC 396
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 CACACGCGTGAACACTATCTCCACCGGCTGGGCTGGCTGCTGCTGCAAGAG 420
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
397 CACACGCGTGAACAGACTCTTCAATGGACAGGACCACTATCTTCTGCTCTGTGG 456
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 GCCTGGTCACTCTGGGAACAGTATCTTTTGGTGGAGAACCATCTCTGCGTCAAGAG 480
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
457 GGCATCACTGTGGCTTAACTCCACCTCTTGAAGAGAGTGTGCTGATCCAGATGGC 516
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 ACGGCGCTCTCTGTGAGACTTCATCTGAGTGGGCAATGGCTGGGATGACATG 540
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
517 CTTGCAAAATGTGTGCATCAGCTTCAGCATCTGCATACCTTCGCGTGGCAGAGCTATG 576
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 TTCAGCTGGAGTCTTTATGCCCCCTGCGCATCATCTTATTTGCTCTTCAAGATTGT 600
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
577 TTTCTCTGGAGTCTCTCTGCCCCCTGGGATCATCTCTGTCTGCTGCGCAGAAATTC 636
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 TGGAGCTGAGCGGAGGAGCAGCTGGGCGACAGGCTCGGATGAAGAGGCGACCCGG 660
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
637 TGGAGCTGCGGAGAG---ACAAATGGACCGGATGCCAAGATCAAGAGAGCCAAACC 693
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
661 TTCATCATGGTGGTGAATTTGTTTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
694 TTCATCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 753
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
721 CTCTATTTCTCTGAGCGGTGGCCCTC-----GAGTGGCTGCGATCCCTCT 765
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
754 ATCCGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
766 GTCCATGGGCGCTGACATAAACCTCAGCTTCACCTACATGAACAGCATGCTGATCCC 825
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
814 GTGAGCTGAGCGTCTCTTATCACTCTCAGCTTCACCTACATGAACAGCATGCTGGAC 873
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
826 CTGCTGATATATTTTCAAGCCCTCTCTTCCCAATTTCTAACAAGCTCAAAATCTGC 885
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
874 GTGGTGTACTACTTCTCCAGGCCATCTTTCCCAACTCTTCTTCCACTTTGATCAACCG 933
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
886 AGTCTGAAACCCCAAGCAGCAGGACACTCAAAA 919
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
934 TGCCTCCAGAGGAGATGACAGGTGAGCCAGATA 967
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RESULT 5
US-07-915-966C-1
; Sequence 1, Application US/07915966C
; Patent No. 568006
; GENERAL INFORMATION:
; APPLICANT: Haddock Dr., John R.
; APPLICANT: Ozenberger Dr., Bradley A.
; APPLICANT: Pausch Dr., Mark H.
; TITLE OF INVENTION: Receptor Identification Method
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: American Home Products Corporation
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,966C
; FILING DATE: 17-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale M.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 31,829-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; PUBLICATION INFORMATION:
; AUTHORS: Haddock Dr., John R.
; AUTHORS: Dr. Ozenberger, Bradley A.
; AUTHORS: Dr. Pausch, Mark H.
; TITLE: Receptor Identification Method
; DATE: 17-JUL-1992
; US-07-915-966C-1
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Query Match      22.1%; Score 229.6; DB 1; Length 545;
Best Local Similarity 65.0%; Pred. No. 7.3e-57;
Matches 356; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

QY 157 TACCTTTTCAATTTGGCGGTGCTGATTTCTCTCTATGATCTGCTGCTTTTGGACA 216
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 TTCGTGGTGAACCTGCTGCGGCTGACTTTCTCTGATCATTTGCTTGGCTTCTGACG 60
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 GACTATTATCTCAGACGTAGACACTGGGCTTTTGGGACATTCCTGCGAGTGGGCTC 276
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 GACAACTATGTCCAGAACTGGGACTGGAGCTTCGGAGCATCCCTGCGCGTATGCTC 120
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
277 TTCAGCTTGGCCATGAACAGGGCCGGAGCATGCTGTTCTTACGTTGGTGGCTGCGGAC 336
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 TTCATGTTGGCCATGAACCGGACAGGCGAGCATCATCTTCTCAGGTGGTGGCTGGAC 180
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
337 AGSTATTTTCAAGTGTGCTCCACCCACCGGCTGAACACTATCTCCACCCGCTGGCG 396
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 AGGTACTTTCAGGTGTGCTCCACCCGCGACCTTCTCTGAACAGATCTCCAAACCGAG 240
QY      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
397 GTGGCATGCTCTGCACCCCTGTGGGCCCTGTCATCTCTGGGAACAGTATCTTTTGTG 456
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CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 07/915,966  
FILING DATE: 17-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Tsevdos Dr., Estelle J.  
REGISTRATION NUMBER: 31,145  
REFERENCE/DOCKET NUMBER: 31829-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-321-2361  
TELEFAX: 203-321-2971  
TELEX: 710-474-4059  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 545 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rat  
PUBLICATION INFORMATION:  
AUTHORS: Hadcock Dr., John R.  
AUTHORS: Dr. Ozenberger, Bradley A.  
AUTHORS: Dr. Pausch, Mark  
TITLE: Receptor Identification Method  
DATE: 17-JUL-1992  
US-08-853-194-1

Query Match 22.1%; Score 229.6; DB 3; Length 545;  
Best Local Similarity 65.0%; Pred. No. 7.3e-57;  
Matches 356; Conservative 0; Mismatches 189; Indels 3; Gaps 1;  
QY 157 TACCTTTTCAATTTGGCCGTGATTTCTCTTATGATTCGCTGCTTTTCGGACA 216  
DB 1 TTCTGCTGTAACCTGTGCGGGCTGACTTCTCTGATCATTTTGTGCGGTCTTGAGC 60  
QY 217 GACTATTACTCAGACGTAGACACTGGGCTTTTGGGAGATTCCTCCGAGTGGGGCTC 276  
DB 62 GACAACTATGTCAGAACTGGGACTGGAGGTTCGGAGCATCCCTTGGCGGTGATGCTC 120  
QY 277 TTCAAGCTTGGCCATGAACAGGGCCGGAGCATCGTCTTCTTACGGTGGTGGTGGAGC 336  
DB 121 TTCAATTTGGCCATGAACCCAGAGGCGAGCATCATCTTCTGACGGTGGTGGTGGAC 180  
QY 337 AGGTATTTCAAAGTGTGTCACCCCAACAGCGGGTGAACTATCTCCACCCGGGTGGCG 396  
DB 182 AGGTATTTCAAGGTGTGTCACCCCAACAGCGGGTGAACTATCTCCACCCGGGTGGCG 240  
QY 397 GCTGGCATGCTTGGACCCCTGTGGGCGCTTGTCTATCTCTGGGAGCATCTTTTGTG 456  
DB 241 GCATCATCTCTGCTTCTTGTGGGAGCATCAGCATCGGCGCTGACATCCACCTCTCTAC 300  
QY 457 GAGAACCATCTCTGCTGCAAGAGACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGC 516  
DB 301 ACGGACATCATGACCCGAAACGGCGATGCAACCTGTGACGAGTTTTAGCATCTCTAC 360  
QY 517 GCAATGGCTGGCATGACATCATGTTCCAGCTGGAGTCTTATGCCCCCTCGGCATCATC 576  
DB 361 ACTTTTCAGGTGGCAGATGCAATGTTCTCTTGGAAATCTTCTGCCCCCTGGGCATCATC 420  
QY 577 TTATTTTGTCTCTTCAAGATGTTTGGAGCTCAGGCGGAGGAGCAGCTGGCGAGACAG 636  
DB 421 CTGTTCTGCTCTGGCAGAGATCATTTGGAGCCTTAAGGAGAG---ACAGATGACAGCAC 477  
QY 637 GCTCGGATGAAGAGCGACCCCGTTTCATCATGGTGGTGGCAATGTGTTTCATCATGC 696  
DB 478 GTCAGATCAAGAGGGCCATCACTTTCATCATGGTGGTGGCAATGTGTTTCATCATGC 537  
QY 697 TACCTGCC 704  
| | | | |

DB 538 TGGCTGCC 545  
RESULT 8  
US-08-955-713-1  
Sequence 1, Application US/08955713  
Patent No. 5955308  
GENERAL INFORMATION:  
APPLICANT: SATHE, GANESH  
APPLICANT: MOONEY, JEFFREY  
APPLICANT: BERGSMAN, DEBK  
APPLICANT: HALSEY, WENDY  
TITLE OF INVENTION: CDNA CLONE HEADS4 THAT ENCODES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,713  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,124  
FILING DATE: 18-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F.  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-70087  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1594 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-955-713-1

Query Match 18.2%; Score 188.8; DB 2; Length 1594;  
Best Local Similarity 54.7%; Pred. No. 8.6e-45;  
Matches 445; Conservative 0; Mismatches 357; Indels 12; Gaps 3;  
QY 53 TGGCGCGCTGCTCATGTGGCTTTGTCTGGGCGCAGTGGCAATGGGTGGCCCTGT 112  
DB 519 TGGCACCACATCTGGCGCTGGAGTTTGTCTGGGCGTGGTGGGAAACAGTTTGGCCCTCT 578  
QY 113 GTGGTTTCTGCTTCCACATGAAGACCTTGAAGCCAGACCTGTTTACCTTTTCAATTGG 172  
DB 579 TCATCTTCTGCAATCCACACGCGGCCCTGGACCTCCAAACGCGTGTCTCTGTCAGCTGG 638  
QY 173 CCGTGGCTGATTTCTCTTATGATCTGCTCTTTCGGACAGACTATTACCTCAGAC 232  
DB 639 TGGCGCTGACTTCTCTCTGATCAGCAACCTGCCCCCTCGCGTGGAGTACTACTCTCTCC 698  
QY 233 GTAGACATCTGGGCTTTTGGGACATTCCTCTGCGAGTGGGCTCTTCACTGTTGGCATGA 292  
DB 699 ATGAGACCTTGGGCTTTGGGCTGCTGCTGCAAGAGTCAACCTCTTCTGCTGTCCACCA 758  
QY 293 ACAGGCGCGGAGCATCGTGTCTTACGTTGGTGGCTGGGACAGATATTTCAAAGTGG 352  
DB 759 ACGGACGCGCGAGGTGTCTTCTCTCAGAGCCATGCACTCAACCCGCTACCTGAGGTGG 818



353 TCCACCCACACCGCGGTGAACACTATCTCCACCGGGTGGCGTGGCATCGTCTGCA 412  
819 TCGACGCCACACGCTGCTGAGCGTGTCTTCTGGGGGAGTGCCTGGGGTGGCGGG 878  
413 CCTGTGGGCGCTGCTCATCTCTGGGAAAGTGTATCTTTTGTGGGAAACCATCTCTGG 472  
879 GACTCTGGG---TGGGATCTCTGCTCTCAACGGGACCTGCTCTGAGCACCTTCTCG 935  
473 TCGAGAGAGCGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCCAATGGGTGGCATG 532  
936 GCGCCCTCTCTGCTCAGCTACAGGGTGGGCAAGAGCCCTCGGCTCGCTCGGCTGGCACC 995  
533 ACATCATGTTCCAGCTGGAGTCTTTATGCGCCCTCGGCATCATCTTATTTGCTCTTCA 592  
996 AGGCACTGATACCTGCTGGAGTCTTCTGCGCATGCGCTCTGCTCTCTT---GCTATTG 1052  
593 AGATTGTTTGGAGCTTGGAGCGGAGGAGCAGAGCTGCGGAGAGGCTCGGATGGAAGAG 652  
1053 TGAGCAATTGGGCTCACCATCCGGAACCGTGTCTGGGCGGGCAGGCGCCGAGAGGG 1112  
653 CGACCGGTTTATCATGCTGGGCAATTTGTTTATCATCATGCTACCTGCGGCGAGGTGT 712  
1113 CCATGCTGTGCTGGGCAATGTTGTTGCTGCGCTCTACACCATCTCTCTTGGCCAGCATCA 1172  
713 CTGCTAGACTCTATTTCTCTGAGACGTTGCTGAGTGCCTCGAGTGCCTCTGTCATG 772  
1173 TCTTGGCATGGCTTCTATGGTGGCTTCTGCGCTGCGGCTGCGGCTCTCTGCACTCT 1232  
773 GGGCGCTGCACTAA-----CCTCAGCTTACCTACATGAACAGAGCTGGATGCC 826  
1233 GCACACAGCTCTTCCATGCTGCTGCGCTTACCTACCTCAACAGTGTCTTGGACCCCG 1292  
827 TGGTGTATTATTTTCAAGCCCTCTCTTCCAA 860  
1293 TGCTCTACTGCTTCTAGCCCCAACTTCTCTCA 1326

## RESULT 9

US-08-955-713-3  
; Sequence 3, Application US/08955713  
; Patent No. 5955308  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: MOONEY, JEFFREY  
; APPLICANT: BERGMA, DEREK  
; APPLICANT: HALSEY, WENDY  
; TITLE OF INVENTION: CDNA CLONE HBOARD54 THAT ENCODES A HUMAN 7-TRANS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/955,713  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050,124  
; FILING DATE: 18-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-76087  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1435 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-955-713-3

Query Match 18.1%; Score 188; DB 2; Length 1435;  
Best Local Similarity 54.1%; Pred. No. 1.4e-44;  
Matches 440; Conservative 3; Mismatches 359; Indels 12; Gaps 3;  
QY 53 TGGCGCGCTGCTCATATGTCCTTTTGTCTGGGCGCACTAGGCAATGGGGTGGCGCTGT 112  
Db 18 TGGCACCAATCTCTGGCCCTGGAGTTTGTCTGGGCGCTGGTGGGAAACAGTTTGGCCCTCT 77  
QY 113 GTGGTCTCTCTCCACATGAAGACCTGGAAGCCCGACACCTGTTTACCTTTTCAATTGG 172  
Db 78 TCATCTCTGCAATCCACACGCGGCCCTGGACCTTCAACACGCTGTTCTCTGCTGAGCTGG 137  
QY 173 CCGTGGCTGATTCTCTCTTATGATCTGCTGCTTTTGGACAGACTATTAATCTCTGAC 232  
Db 138 TGGCGCTGACTCTCTCTGATCAGCAACCTGCGCCCTCGCGTGGACTACTACTCTCTCTCC 197  
QY 233 GTAGACACTGGGCTTTTGGGACATTCCTTGGCGAGTGGGGCTCTTACGTTGGCCATGA 292  
Db 198 ATGAGACCTTGGCGCTTTGGGGCTGCTGCTTGAAGTCAACCTCTTCTGCTGTCNACCA 257  
QY 293 ACAGGCGCGGAGCATCGTGTCTTACGCTGGTGGCTGGGAGCAGAGTATTTCAAAGTGG 352  
Db 258 ACCGCAAGCGAGGTGTCTTCTTACAGCCATCGCACTCAACCGCTACCTGAGGTGG 317  
QY 353 TCCACCCCGCCACCGGGTGAACACTATCTCCACCGGGTGGCGCTGGGCAATGCTCTGCA 412  
Db 318 TGCANCCCCACACGCTGTGAACCGTGTCTTGGTGGGGGCACTGCGGGTGGNCGGG 377  
QY 413 CCTGTGGGCGCTGCTCATCTTGGGACAGTGTATCTTTTGTGGGAGAACCATCTCTGG 472  
Db 378 GAATCTGGG---TGGGCACTCTCTGCTCTCAACGGGNAACCTGCTCTGAACACCTTCTCG 434  
QY 473 TGCAAGAGACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCAAATGGCTGGCATG 532  
Db 435 GCGCTCTCTGCTGCTAGCTAGGGTGGGACGACACCTCGGCTCGCTCGCTGGCACC 494  
QY 533 ACATCATGTTCCAGCTGGAGTCTTATGCGCCCTCGGCACTCATCTTATTTGCTCTCTTCA 592  
Db 495 AGGCACCTGTACTGCTGAGTTTCTCTGCGCACTGGCGCTCATCTCTTT---GCTATTG 551  
QY 593 AGATTGTTTGGAGCTTGGCGGAGGAGCAGAGCTGGCCAGACAGCTCGGATGAGAGG 652  
Db 552 TGAGCAATTGGGCTCAACATCCGGAACCGTGTCTTGGGCGGGCAGGAGCCCGCAGAGGG 611  
QY 653 CGACCGCGTTTCATCATGCTGTGCAATTTCTGTTTCATCATGCTACTGCTCCAGCGCTGT 712  
Db 612 CCATGCTGTGCTGGCCATGTTGGTGGCTGTCTACACCACTGTTCTTGGCCAGCATCA 671  
QY 713 CTGCTAGACTCTTATTTCTCTGAGCGGTGCCCTCGAGTGGCTGGATGCTCTCTCTCATG 772  
Db 672 TCTTTGGCATGGCTTCCATGGTGGCTTTCTGGGCTGTCCGCTGCGGATCTCTGACCTCT 731  
QY 773 GGGCGCTGCACTAA-----CCTCAGCTTCACTACATGAACAGCATGCTGATCCCC 826  
Db 732 GCACACAGCTCTTCCATGGCTGCTGCGCTTACCTTACCTCAACAGAGTCTCTGACCCCG 791  
QY 827 TGGTGTATTATTTTCAAGCCCTCTCTTCTCCAA 860  
Db 792 TGCTCTACTGCTTCTAGCCCCAACTTCTCTCA 825

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RESULT 10
US-09-130-749-1
; Sequence 1, Application US/09130749
; Patent No. 6031090
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-AUG-1998
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-130-749-1
Query Match 13.4%; Score 139.2; DB 3; Length 960;
Best Local Similarity 51.4%; Pred. No. 1.6e-30;
Matches 427; Conservative 0; Mismatches 388; Indels 15; Gaps 4;
QY 62 TGCTCATGTGGCTTTGTGCTGGGCGCCTAGGCAATGGGTGCGCCCTGTGTTCT 121
DB 59 TGCTGGGCTGGAGTGGGCTGGTCTGCTGGGCAACGGGTGGCGCTTGGACCTTC 118
QY 122 GCTTCCACATGAGACTGAGCCAGCCAGCACTGTTACCTTTTCAATTTGCCGTGCTG 181
DB 119 TGTTCGGGTGAGGTGGAGCCGTACGCTGTCTACCTGCTCAACTGGCCCTGGCTG 178
QY 182 ATTTCTCTCTATGATCTGCTGCTTTTTCGGACAGACTATTACCTCAGACGTAGACACT 241
DB 179 ACCTGCTGTTGGCTGGCTGCTGCTTCTTCTGGCGCCTTCTACCTGAGCCTCCAGGCTT 238
QY 242 GGGCTTTTGGGACATTCCTTCCGAGTGGGCTTCTTCACTGGCCATGACAGGCGCG 301
DB 239 GGCATCTGGGCGGTGGCTGCTGGGCGCTTCTTCTGGCGCCTTCTACCTGAGCCTCAGCGCG 298
QY 302 GGAGCATCGTCTCTTACGCTGTGCTGGGAGGTATTTCAAAAGTGTCTCACCCCG 361
DB 299 TGGGATGGCTTCTTGGCGCGGTGGCTTGGACCGGTACCTCGTGTGGTCCACCTC 358
QY 362 ACCACGCGGTGAACACTATCTTCCACCGGGGTGGCGGCTGGCATGCTGTGCACTCTG 421
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359 GGCTTAAGGTCAACCTGCTGCTCTCTCAGGCGGCGCTCGGGGCTCTCGGGCTCTGCTGGC 418

422 CCCTGCTCATCTGGAACAGTGTATCTTTTCTGGAGAACCATCTCTCTGGTGCAGAGA 481

419 TCCTGATGTGCGCCCTCACTGCGCGCGGCTTGTCTATCTCTGAGGCGGCCAGAACTCCA 478

482 CGGCGCTCTCTGAGAGCTTTCATCATGGAGTCGGC-----CAATGGCTGGCATGACA 535

479 CAGGTGCGCAGATTCTTACTCCAGGCGAGAGCGCTCTCTCAGCATCATCTGGCAGGAAG 538

536 TCATGTTCCAGCTGGAGTCTTTATGCCCCCTCGGCAATCATCTTATTTTGTCTCTTCAAGA 595

539 CACTCTCTGCTTCACTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 598

596 TTGTTTGGAGCTGAGCGGAGG---CAGCAGCTGGCCAGACAGGCTCGGATGAGAGAGG 652

599 TCATCAGGCTCTCCAGAAAGACTCCGGAGCGCTGAGAAACAGCCAGCTTCAGCGGG 658

653 CGACCGGTTTCATGTTGGTGGCAATTTGTTTCATCATCATCTACCTGCCCGGCTGT 712

659 CCAGGCACTGGTCACTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 718

713 CTGCTAGACT-CTAATTCCTCTGGACGGTGGCTCGAGTGGCTCGAGTCCCTCTGTCCAT 771

719 TGGCCAGAGTCTGATGACATCTTCCAGAACTCTGGGAGCTGCGGGGCTTTTGTGCGAG 778

772 GGGGCGCT----GCACATAACCTCAGCTTACCTACATGAGAACAGCATGCTGGATCCCC 826

779 TGCTCATACCTCGGATGTCAGGGCAGCTCACTACCTGCGACAGTGTCTCAACCCCG 838

827 TGGTGTATTATTTTCAAGCGCTCTTCCCAAAATCTTCAACAAGCTC 876

839 TGGTATAGTCTTCTCAGCGCCCTTTCAGGAGCTCTATCGAGGCTC 888

RESULT 11

US-09-130-749-1

; Sequence 1, Application US/09130749

; Patent No. 6031344

; GENERAL INFORMATION:

; APPLICANT: SHABON, USMAN

; APPLICANT: ELISHOURBAGY, NABIL

; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM

; TITLE OF INVENTION: RECEPTOR (GPR31A)

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/130,749

; FILING DATE: 07-AUG-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GP-70513

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 960 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-130-749-1

Query Match 13.4%; Score 139.2; DB 3; Length 960;

Best Local Similarity 51.4%; Pred. No. 1.6e-30;

Matches 427; Conservative 0; Mismatches 388; Indels 15; Gaps 4;

QY 62 TGCTCATGTGGCTTTGTGCTGGGCGCCTAGGCAATGGGTGCGCCCTGTGTTCT 121

DB 59 TGCTGGGCTGGAGTGGGCTGGTCTGCTGGGCAACGGGTGGCGCTTGGACCTTC 118

QY 122 GCTTCCACATGAGACTGAGCCAGCCAGCACTGTTACCTTTTCAATTTGCCGTGCTG 181

DB 119 TGTTCGGGTGAGGTGGAGCCGTACGCTGTCTACCTGCTCAACTGGCCCTGGCTG 178

QY 182 ATTTCTCTCTATGATCTGCTGCTTTTTCGGACAGACTATTACCTCAGACGTAGACACT 241

DB 179 ACCTGCTGTTGGCTGGCTGCTGCTTCTTCTGGCGCCTTCTACCTGAGCCTCCAGGCTT 238

QY 242 GGGCTTTTGGGACATTCCTTCCGAGTGGGCTTCTTCACTGGCCATGACAGGCGCG 301

DB 239 GGCATCTGGGCGGTGGCTGCTGGGCGCTTCTTCTGGCGCCTTCTACCTGAGCCTCAGCGCG 298

QY 302 GGAGCATCGTCTCTTACGCTGTGCTGGGAGGTATTTCAAAAGTGTCTCACCCCG 361

DB 299 TGGGATGGCTTCTTGGCGCGGTGGCTTGGACCGGTACCTCGTGTGGTCCACCTC 358

QY 362 ACCACGCGGTGAACACTATCTTCCACCGGGGTGGCGGCTGGCATGCTGTGCACTCTG 421







Db 576 TSCCCTGGTCTCCAGTGGGCTTCACTTCCCGTTTCATCCACAGGTCACCTGCTA 635  
Qy 588 CTTCAAGATTGTTTGGAGCCTGAGCGGAGCAGCAGCTGGCCAGACAGGCTCGGATGAA 647  
Db 636 CTTGCTGATCATCGCAGCCTGCGCAGGCGCTGCTGTGGAGAGCGCCTCAAGACCAA 695  
Qy 648 GAAGGCGACCGGTTTCATCATGTTGGTGGCAATGTT-----GTTTCATCATGCTA 698  
Db 696 GCGAGTGGGATGATGCCATAGTGGCCATCTTCTGGTCTGCTTGGTGGCCCTACCA 755  
Qy 699 CTTGCCAGCGGTGCTGCTAGACTCTATTTCTCTGGACGCTGCTCGAGTGGCTGCGA 758  
Db 756 CGTCAACCGTCCGCTACGCTGCTGCTACCGGAGCCATGGGGCTCTCTGGCCACCA 815  
Qy 759 TCCCTCTGTCCATGGGCGCTGCAATACCACTCAGCTTCACTTCAATGAAACAGCTCT 818  
Db 816 GCGCATCTCGCCCTGGCAACCGCATCACCTCTGCTCACCAGCCTCAACGGGGCACT 875  
Qy 819 GATCCCTCGGTGATTTT 839  
Db 876 CGACCCCATCATGATTTCTT 896

## RESULT 15

US-09-016-434-1484  
Sequence 1484, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1484:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1900 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: G992699  
US-09-016-434-1484

Query Match 10.5%; Score 109; DB 4; Length 1900;  
Best Local Similarity 47.1%; Pred. No. 1.3e-21;

Matches 377; Conservative 0; Mismatches 415; Indels 9; Gaps 1;  
Qy 48 GGTGATGTCGGCGCTGCTCATTTGGCTTTGCTGGCGGACCTAGGCAATGGGTCGC 107  
Db 795 GCTGTTCCGCTCTCTTACCTTCTGGATTTTATCTGGCTTTAGTGTGGCAATACCTGCG 854  
Qy 108 CTTGTGGTGTTCCTGCTTCCACATGAAGACCTGGAAGCCAGACACTGTTTATCTTTTCAA 167  
Db 855 TCTGTGGCTTTTCATCGAGACCAAGTCGGGACCCCGGCAACAGTGTTCCTGATGCA 914  
Qy 168 TTGGCGCTGCTGCTGCTTCTCTTATGATGCTGCTGCTTTTGGACAGACTATTAATCT 227  
Db 915 TCTGCGCTGGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974  
Qy 228 CAGACGTAGACACTGGGCTTTTGGGCAATTTCCCTGCGAGTGGGCTCTTCACTGCTGC 287  
Db 975 CTCTGGGAACCACTGGGCAATTTGGGGAATCGCAGTGGCTCTCACCGGCTTCTCTCTTA 1034  
Qy 288 CATGAACAGGCGCGGAGCATGCTTCTTACGCTGGTGGCTGGGACAGTATTTCAA 347  
Db 1035 CTTCAACATGTAACGCGAGCATCTACTTCTCACCTGCTACAGCGCGACCGTTTCTGCG 1094  
Qy 348 AGTGTCCACCCCAACGCGGTGAACATATCTCCACCCGCGGTGGCGGTGGCGATGCT 407  
Db 1095 CATTTGTCACCGCGTCAAGTCCCTCAAGCTCGGAGGCGCTCTACGCAACACTGGCGTG 1154  
Qy 408 CTGCACCTGTGGCGCTTGGTCTATCTGGGGAACAGTGTATCTTTTGTGGAGAACATCT 467  
Db 1155 TGCCTTCTGTGGGTGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1214  
Qy 468 CTGGTGCAGAGACGGCGCTCTCTGTGAGAGCTTTCATGAGTGGAGTGGGCAATGGCTG 527  
Db 1215 GGTGAGACCAACCAACAGCGTGTGCTGCTGAGCTGTACCGGAGAGAGCGCTCCCAACA 1274  
Qy 528 SCATGACATCATGTTCCAGCTGGAGTCTTTTANGCCCTCGGCAATCATCTTATTTTGTCT 587  
Db 1275 TGCCCTGTGCTCCCTGGCAGTGGCTTCACTTCCGTTTCATCACCGGTCACTGCTTA 1334  
Qy 588 CTTCAAGATTGTTGGAGCCTGAGCGGAGGAGCAGCTGGCCAGAGGCTCGGATGAA 647  
Db 1335 CTTGATCATTCGCGAGCTGGCGAGGCGCTGGTGTGGAGAGGCGCTCAAGACCA 1394  
Qy 648 GAAGCGACCGGTTTCATGCTGGTGGCAATTTGT-----GTTTCATCATGCTA 698  
Db 1395 GCGAGTGGCATGATGCCATAGTGTGCTGGCCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1454  
Qy 699 CTTGCCAGCGTGTGCTAGACTCTATTTCTCTGGAGCGGTGGCGCTCGAGTGGCTGCGA 758  
Db 1455 CGTCAACCGCTCCCTTACGCTGCTGCACTACCGAGCCATGGGGCTCTCTGGCCACCA 1514  
Qy 759 TCCCTCTGTCCATGGGCGCTGCACTAACCTCAGCTTTCACCTACATGAACAGCATGCT 818  
Db 1515 GCGCATCTGCGCTGGCCCTGGCAACCGGATCACCTCTGCTTCCAGGCTTCAACGGGCACT 1574  
Qy 819 GGATCCCTCGGTGATTTT 839  
Db 1575 CGACCCCATCATGATTTCTT 1595

Search completed: July 3, 2004, 08:44:43  
Job time : 110 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: July 3, 2004, 06:00:01 ; Search time 3245 Seconds  
(without alignments)  
9552.217 Million cell updates/sec

Title: US-10-076-260-1  
Perfect score: 1038  
Sequence: 1 agtacaacgggtcgctg.....ccacattgtgagtgccac 1038

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpi:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pig:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038	100.0	1372	11	AF345568 Homo sapi
2	722.8	69.5	3028	11	AK029064 Mus muscu
3	711.8	68.6	3283	11	AK046700 Mus muscu
4	705.4	68.0	792	14	CD559495 AGENCOURT

C	5	676	65.1	786	14	CD559498
C	6	672.8	64.8	793	14	CD559497
C	7	669.4	64.5	790	14	CD559496
C	8	619.8	59.7	773	14	CD559653
	9	600	57.8	748	14	CD559650
	10	591.4	57.0	743	14	CD559651
	11	584.4	56.3	731	14	CD559652
	12	558.6	53.8	1004	14	CD246157
C	13	453.8	43.7	594	29	CE432388
	14	443.8	42.8	635	14	CB576966
	15	370.8	35.7	2146	11	BC027965
	16	369.2	35.6	2059	11	BC056419
	17	367.6	35.4	2068	11	BC047891
	18	324.6	31.3	1201	9	AL545172
	19	317.2	30.6	960	9	AL546894
	20	309.2	29.8	1057	12	BM918711
	21	309	29.8	801	12	BI837965
	22	307	29.6	1076	12	BM923028
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	24	300.8	29.0	472	14	CB730514
	25	289.4	27.9	1201	9	AL554198
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	36	224.2	21.6	690	14	CD690497
	37	220.2	21.2	645	14	CD469236
	38	218.2	21.0	550	10	BF074336
	39	217.2	20.9	1082	13	BQ710754
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	42	215.8	20.8	636	12	BI489649
	43	215.2	20.7	614	14	CD468367
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## ALIGNMENTS

RESULT 1	AF345568	1372 bp	linear	HTC 02-MAY-2003
LOCUS	Homo sapiens putative chemokine receptor (FKSG80) mRNA, complete cds.			
DEFINITION	AF345568.1 GI:13517963			
ACCESSION	AF345568			
VERSION	AF345568.1			
KEYWORDS	HTC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 1372)			
AUTHORS	Alberta, E.O., Petersen, R.H., Hughes, K.W. and Lechner, B.			
TITLE	Miscellaneous notes on Pleurotus			
JOURNAL	Persoonia 18, 55-69 (2002)			
REFERENCE	2 (bases 1 to 1372)			
AUTHORS	Wang, Y.-g. and Gong, L.			
TITLE	Molecular cloning of FKSG80, a novel gene encoding a putative chemokine receptor			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 1372)			
AUTHORS	Wang, Y.-g.			
TITLE	Direct Submission			
JOURNAL	Submitted (06-FEB-2001) Beijing FENGKESHENG Function Gene Technology Ltd., 4 Tou Tiao Lu Chang Street, Xuanwu District, Beijing 100050, P.R. China			

Db	802	TTTCATCATGGTGTGGCAATTGTGTTTCATCACATGCTACCTGCGCCAGCGGTGTCGTGAGA	861	
Qy	721	CTCTATTTCCTCTGGA	CGGTGCTTCAGTGGCTTCGGATCCCTCTGTCATCGGGGCGCTG	780
Db	862	CTCTATTTCCTCTGGA	CGGTGCTTCAGTGGCTTCGGATCCCTCTGTCATCGGGGCGCTG	921
Qy	781	CACATAACCCCTCAGCTTCACCTACATCAACAGCATGCTGGATCCCTCGTGGTGTATTTT	840	
Db	922	CACATAACCCCTCAGCTTCACCTACATCAACAGCATGCTGGATCCCTCGTGGTGTATTTT	981	
Qy	841	TCAAGCGCCCTCTTTCCTCAAAATCTCAACAAGCTCAAAATCTGAGTCTGAAACCCCAAG	900	
Db	982	TCAAGCGCCCTCTTTCCTCAAAATCTCAACAAGCTCAAAATCTGAGTCTGAAACCCCAAG	1041	
Qy	901	CAGCCAGCAGCACTCAAAACACAAAGCCGAGAGATGCCAATTTGCAACCTCGTCTGC	960	
Db	1042	CAGCCAGCAGCACTCAAAACACAAAGCCGAGAGATGCCAATTTGCAACCTCGTCTGC	1101	
Qy	961	AGGAGTTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCC	1020	
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RESULT 2				
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LOCUS	AK029064	3028 bp	mRNA linear HTC 18-SEP-2003	
DEFINITION	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:473248A1.8 product:similar to PUTATIVE CHERMOKINE RECEPTOR (G PROTEIN-COUPLED RECEPTOR) [Homo sapiens], full insert sequence.			
ACCESSION	AK029064			
VERSION	AK029064.1	GI:263225037		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Fujimoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yamawake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076851			
REFERENCE				
AUTHORS				
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
JOURNAL	Functional annotation of a full-length mouse cDNA collection			
MEDLINE	Nature 409, 685-690 (2001)			
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REFERENCE				
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AUTHORS				
TITLE				
JOURNAL				





AK046700 3283 bp mRNA linear HTC 20-SEP-2003  
 LOCUS Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length  
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 CHEMOKINE RECEPTOR (G PROTEIN-COUPLED RECEPTOR) [Homo sapiens],  
 full insert sequence.  
 AK046700  
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 VERSION AK046700.1  
 KEYWORDS H7C; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
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 Genome Res. 10 (10), 1617-1630 (2000)  
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 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,  
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 RIKEN integrated sequence analysis (RISA) system--384-format  
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 Genome Res. 10 (11), 1757-1771 (2000)  
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 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3283)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Yuramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan [E-mail: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216]  
 cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

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QY 1032 GTGGCAC 1038
Db 39 GTGGCAC 33

RESULT 5
CD559498/c
LOCUS
DEFINITION
AGENCOURT_14496820 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971816 5', mRNA sequence.
CD559498
CD559498.2 GI:38453562
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
On Jun 10, 2003 this sequence version replaced gi:31585566.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://images.llnl.gov
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complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
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Db 765 GGCCTGGAGCATCTCTCTTACGCTGGTGGTGGGACAGGATTT--CAAAGTGTCCA 710

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FEATURES  
source

ORIGIN

Query Match 65.1%; Score 676; DB 14; Length 786;  
Best Local Similarity 98.0%; Pred. No. 8.1e-171;  
Matches 717; Conservative 0; Mismatches 10; Indels 5; Gaps 3;  
QY 297 GGCCTGGAGCATCTCTCTTACGCTGGTGGTGGGACAGGATTTCAAGTGTCCA 356  
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RESULT 6  
CD559497/c  
LOCUS  
DEFINITION  
AGENCOURT\_14496881 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971817 5', mRNA sequence.  
CD559497  
CD559497.2 GI:38453561  
EST.  
SOURCE  
Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 793)  
NIH-MGC http://mgi.nci.nih.gov/  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
On Jun 10, 2003 this sequence version replaced gi:31585565.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat

CD559497 793 bp mRNA linear EST 19-NOV-2003  
AGENCOURT\_14496881 NIH\_MGC\_195 Homo sapiens cDNA clone  
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TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
On Jun 10, 2003 this sequence version replaced gi:31585565.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat

cdNA Library Preparation: Bhat Laboratory  
 cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
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 available from NCBI's RefSeq). Template for PCR is cdNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)  
 a Note: this is a NIH MGC Library."

## ORIGIN

Query Match 64.8%; Score 672.8; DB 14; Length 793;  
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 Matches 715; Conservative 0; Mismatches 12; Indels 5; Gaps 3;

QY 297 GCGCGGAGCATCGTGTCTCTTACCGTGTGGCTGCGGACAGATATTTCAAAGTGTGCA 356  
 Db 766 GCGCGGAGCATCGTGTCTCTTACCGTGTGGCTGCGGACAG--TATTTCAAAGTGTGCA 711

QY 357 CCCCACACACCGGTGAACATCTTCCACCGGTGGCGGTGGCATCGTCTGCACCT 416  
 Db 710 CCCCACACACCGG--GAACATCTTCCACCGGTGGCGGTGGCATCGTCTGCACCT 652

QY 417 GTGGGCCCTGTCTATCTCTGGGAACAGTGTATCTTTTGTGGAGAACCATCTCTGGTGCA 476  
 Db 651 GTGGGCCCTGTCTATCTCTGGGACAGTGTATCTTTTGTGGAGAACCATCTCTGGTGCA 592

QY 477 AGAGAGCGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCATGAGTGGCATGACAT 536  
 Db 591 AGAGAGCGCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCATGAGTGGCATGACAT 532

QY 537 CATGTTCCAGCTGGAGTCTTTATGCCCCCTCGGATCATCTTATTTTGTCTCTTCAAGAT 596  
 Db 531 CATGTTCCAGCTGGAGTCTTTATGCCCCCTCGGATCATCTTATTTTGTCTCTTCAAGAT 472

QY 597 TGTTTGGAGCCTGAGCGGCGAGCAGCTGGCCAGACAGCTCGGATGAAGAGGCGAC 656  
 Db 471 TGTTTGGAGCCTGAGCGGCGAGCAGCTGGCCAGACAGCTCGGATGAAGAGGCGAC 412

QY 657 CCGGTTATCATGAGTGGCAATGTGTTTCATCATGCTACCTGCCAGCGTGTCTGCG 716  
 Db 411 CCGGTTATCATGAGTGGCAATGTGTTTCATCATGCTACCTGCCAGCGTGTCTGCG 352

QY 717 TAGACTCTATTTCTCTGACGCTGCCCTCGAGTGCCTGCGATCCCTCTGTGTCATGGGCG 776  
 Db 351 TAGACTCTATTTCTCTGACGCTGCCCTCGAGTGCCTGCGATCCCTCTGTGTCATGGGCG 292

QY 777 CTTGCAATACCTCCTAGCTTCACTACATGAAACAGCATGCTGGATCCCTGGTGTATTA 836  
 Db 291 CTTGCAATACCTCCTAGCTTCACTACATGAAACAGCATGCTGGATCCCTGGTGTATTA 232

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QY 957 TCCAGGAGTTGCATCATGCTGTGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGA 1016  
 Db 111 TCCAGGAGTTGCATCATGCTGTGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGA 52

QY 1017 TCCCCACATTTGT 1028  
 Db 51 TCCCCACATTTGT 40

## RESULT 7

CD559496/c  
 LOCUS  
 DEFINITION  
 AGENCOURT\_14497010 NIH\_MGC\_195 Homo sapiens cdNA clone  
 IMAGE:6971819 5', mRNA sequence.

## ACCESSION

CD559496  
 VERSION  
 KEYWORDS  
 SOURCE

## ORGANISM

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC <http://imgc.nci.nih.gov/>  
 1 (bases 1 to 790)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585564.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 cdNA Library Preparation: Bhat Laboratory  
 cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRBK2 row: c column: 10  
 High quality sequence stop: 703.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

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 /note="Vector: pDNR-Dual; Site 1: loxP-SalI; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cdNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat) a Note: this is a NIH\_MGC Library."

## ORIGIN

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Query Match      64.5%; Score 669.4; DB 14; Length 790;
Best Local Similarity 97.6%; Pred. No. 4.9e-169;
Matches 590; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 328 GCTCGGACAGGTATTCAAGTGTGTCCACCCACCGCGGTGAACACATATCTCCACC 387
D 735 GGTCTGCGACAGGTATTCAAGTGTGTCCACCCACCGCGGTGAACACATATCTCCACC 577
QY 388 CGGCTGGCGGCTGGCATGCTGTCACCTCTGGGCGCTGGTCACTCTGGGAACAGTGTAT 447
D 676 CGGCTGGCGGCTGGCATGCTGTCACCTCTGGGCGCTGGTCACTCTGGGAACAGTGTAT 617
QY 448 CTTTGTCTGGAGAACCATCTCTGCTGCAAGAGCGCGCTCTCTGTGAGAGCTTCATC 507
D 616 CTTTGTCTAGAGAACCATCTCTGCTGCAAGAGCGCGCTCTCTGTGAGAGCTTCATC 557
QY 508 ATGAGTCTGGCAATGGCTGGCATGACATCATGTTCCAGCTGGAGTCTTATGCCCCC 567
D 556 ATGAGTCTGGCAATGGCTGGCATGACATCATGTTCCAGCTGGAGTCTTATGCCCCC 497
QY 568 GGCATCATCTTATTTTGTCTCTTCAAGTATGTTGGAGCGCTGGAGCGGAGCGAGCTG 627
D 496 GGCATCATCTTATTTTGTCTCTTCAAGTATGTTGGAGCGCTGGAGCGGAGCGAGCTG 437
QY 628 GCCAGACAGGCTCGGATCAAGAGCGCGCTTCATCATGTTGGTGGCAATTTGTGTC 687
D 436 GCCAGACAGGCTCGGATCAAGAGCGCGCTTCATCATGTTGGTGGCAATTTGTGTC 377
QY 688 ATCATGCTACTGCTGCCAGCGTGTCTAGACTTATTTCTCTGAGCGTGGCCCTCG 747
D 376 ATCATGCTACTGCTGCCAGCGTGTCTAGACTTATTTCTCTGAGCGTGGCCCTCG 317
QY 748 AGTCCCTGCGATCCCTCTGCTCCAGCGCGCTTCATCATGTTGGTGGCAATTTGTGTC 807
D 316 AGTCCCTGCGATCCCTCTGCTCCAGCGCGCTTCATCATGTTGGTGGCAATTTGTGTC 257
QY 808 AACAGCATGCTGGATCCCTGCTGTATTTATTTTCAAGCGCGCTCTCTTCCCAATTTCTAC 867
D 256 AACAGCATGCTGGATCCCTGCTGTATTTATTTTCAAGCGCGCTCTCTTCCCAATTTCTAC 197
QY 868 AACAGCATGCTGGATCCCTGCTGTATTTATTTTCAAGCGCGCTCTCTTCCCAATTTCTAC 927
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LOCUS
DEFINITION AGENCOURT 14496792 NIH MGC 195 Homo sapiens cDNA clone
IMAGE: 6971816 5', mRNA sequence.
CD559653
VERSION CD559653.2 GI:38559026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 773)
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585721.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm0D07 Bethesda, MD 20892  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Cloned by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRBK2 row: c column: 07  
High quality sequence start: 9  
High quality sequence stop: 740.

FEATURES  
source

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/clone\_lib="NIH\_MGC\_195"  
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loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[http://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
a Note: this is a NIH\_MGC Library."

## ORIGIN

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Query Match      59.7%; Score 619.8; DB 14; Length 773;
Best Local Similarity 98.6%; Pred. No. 1.2e-155;
Matches 624; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTATGCCGCG 60
D 141 ATGTACAAAGGTCGTGCTGCCGATCGAGGGGACACCATCTCCAGGTATGCCGCG 200
QY 61 CTGCTCATTTGGGCTTTGTCTGGCGCACTAGGCGGTCGCGCTGTCGTTTC 120
D 201 CTGCTCATTTGGGCTTTGTCTGGCGCACTAGGCGGTCGCGCTGTCGTTTC 260
QY 121 TGCTTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCGGTGGCT 180
D 261 TGCTTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCGGTGGCT 320
QY 181 GATTTCTCTTATGATCTGCTGCCCTTTTCGACAGACATATTAACCTCAGACGTAGACAC 240
D 321 GATTTCTCTTATGATCTGCTGCCCTTTTCGACAGACATATTAACCTCAGACGTAGACAC 380
QY 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 300
D 381 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 440
QY 301 GGGAGCATCGTGTTCCTTACGTTGGTGGTCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360
D 441 GGGAGCATCGTGTTCCTTACGTTGGTGGTCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 500
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Db 441 GCGAGCATGCTGCTTCCCTACGGTGGTGGCTGGGACACAGCTATTTCACAGTGGTCCACCCC 500

QY 361 CACACGGGCTGAACACATCTCCACCCGGGCTGGGCTGGCATGCTCTGCAACCTGTGG 420

Db 501 CACACGGGCTGAACACATCTCCACCCGGGCTGGGCTGGCATGCTCTGCAACCTGTGG 560

QY 421 GCGCTGGTCTATCTGCGACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGCAGAG 480

Db 561 GCGCTGGTCTATCTGCGACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGCAGAG 620

QY 481 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGGCCAATGGCTGGCATGACATCATG 540

Db 621 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGGCCAATGGCTGGCATGACATCATG 680

QY 541 TTCAGCTGGAGTCTTTATGCCCCCTCGCATCATCTATTATTTGCTTCCCTTCAGATTGTT 600

Db 681 TTCAGCTGGAGTCTTTATGCCCCCTCGCATCATCTATTATTTGCTTCCCTTCAGATTGTT 740

QY 601 TGGAGCCTGAGCGGAGGAGCAGCTGGCCAGA 633

Db 741 TGGAGCCTGANNGCGAAGCAGCAGCTGGCCAGA 773

RESULT 9

CD559650

LOCUS

DEFINITION

AGENCOURT\_14497045 NIH\_MGC\_195 Homo sapiens CDNA clone

IMAGE:6971820 5', mRNA sequence.

CD559650

VERSION

CD559650.2 GI:38559022

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 748)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585718.

Contact: Daniela S. Gerhardt, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Narayan Bhat

CDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: IRBK2 row: C column: 11

High quality sequence start: 11

High quality sequence stop: 745.

Location/Qualifiers

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/db\_xref="taxon:9606"

/clone="IMAGE:6971820"

/tissue\_type="mixed"

/lab\_host="DH5A (T1 phage-resistant)"

/clone\_lib="NIH MGC 195"

/note="Vector: pDNR-Dual; Site\_1: loxp-SalI; Site\_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites

FEATURES

source

of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearrayed\\_plates/IRBK\\_presV.dat](http://image.llnl.gov/image/rearrayed_plates/IRBK_presV.dat)

a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 57.8%; Score 600; DB 14; Length 748;  
Best Local Similarity 99.2%; Pred. No. 2.5e-150;  
Matches 603; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 141 ATGTACAAAGGCTGTGCTGCGCATCGAGAGGAGGACACCATCTCCAGGTGATGCGCGCG 200

QY 61 CTGCTCATTTGGCCCTTTGTGCTGGGCGCACTAGGCAATGGGCTGCCCTGTGTGGTTTC 120

Db 201 CTGCTCATTTGGCCCTTTGTGCTGGGCGCACTAGGCAATGGGCTGCCCTGTGTGGTTTC 260

QY 121 TGCCTCCACATGAAGACCTGGAAGCCAGCACCTGTTTACCTTTCAATTTGGCCGTGGCT 180

Db 261 TGCCTCCACATGAAGACCTGGAAGCCAGCACCTGTTTACCTTTCAATTTGGCCGTGGCT 320

QY 181 GATTTCTCTCTATGATCTGCTGCTTTTGGAGACAGCTATTACCTCAGACGTAGACAC 240

Db 321 GATTTCTCTCTATGATCTGCTGCTTTTGGAGACAGCTATTACCTCAGACGTAGACAC 380

QY 241 TGGGCTTTTGGGAGACATTCCTCGCGAGTGGGCTCTTCACGTTGGCCATGAACAGGCCC 300

Db 381 TGGGCTTTTGGGAGACATTCCTCGCGAGTGGGCTCTTCACGTTGGCCATGAACAGGCCC 440

QY 301 GGGAGCATGCTGTTCTTACGGTGGTGGCTGGGAGCAGCTATTTCAAAGTGGTCCACCCC 360

Db 441 GGGAGCATGCTGTTCTTACGGTGGTGGCTGGGAGCAGCTATTTCAAAGTGGTCCACCCC 500

QY 361 CACGAGGGGTHACACATCTCTCCACCCGGTGGGCGCTGGCATCGTCTGCACCCCTGTGG 420

Db 501 CACGAGGGGTHACACATCTCTCCACCCGGTGGGCGCTGGCATCGTCTGCACCCCTGTGG 560

QY 421 GCGCTGGTCTATCTGCGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGCAGAG 480

Db 561 GCGCTGGTCTATCTGCGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGCAGAG 620

QY 481 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGGCCAATGGCTGGCATGACATCATG 540

Db 621 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGGCCAATGGCTGGCATGACATCATG 680

QY 541 TTCAGCTGGAGTCTTTATGCCCCCTCGCATCATCTATTATTTGCTTCCCTTCAGATTGTT 600

Db 681 TTCAGCTGGAGTCTTTATGCCCCCTCGCATCATCTATTATTTGCTTCCCTTCAGATTGTT 740

QY 601 TGGAGCCT 608

Db 741 TGGAGCCT 748

RESULT 10

CD559651

LOCUS

DEFINITION

AGENCOURT\_14496981 NIH\_MGC\_195 Homo sapiens CDNA clone

IMAGE:6971819 5', mRNA sequence.

CD559651

VERSION

CD559651.2 GI:38559023

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 743)

NIH-MGC <http://mgc.nci.nih.gov/>.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** On Jun 10, 2003 this sequence version replaced gi:31585719.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs@mail.nih.gov  
 Tissue procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: IRBK2 row: c column: 10  
 High quality sequence stop: 728.

**FEATURES**  
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 /tissue\_type="mixed"  
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 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat)  
 a Note: this is a NIH\_MGC Library."

**ORIGIN**  
 Query Match 57.0%; Score 591.4; DB 14; Length 743;  
 Best Local Similarity 99.5%; Pred. No. 5.le-14b;  
 Matches 614; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

1 ATGTACAAACGGGTGTGTGTCGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60  
 111 ATGTACAAACGGGTGTGTGTCGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 170  
 61 CTGCTCATTTGGGCTTTGTGTCGGGCGCACTAGGCAATGGGGTGCCTGTGTGTTTC 120  
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 121 TGCTTCACATGAAGACCTGAAGCCGACGACTGTTTACCTTTCAATTTGGCCGTGGCT 180  
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 291 GATTTCCTCTTATGATCTGCTGCTGCTTTTGGACAGACTATTACTCAGACGTAGACAC 350  
 241 TGGGCTTTTGGGACATTCCTTGCAGAGTGGGGCTCTTTCAGTTGGCCGACAAAGAGGCC 300  
 351 TGGGCTTTTGGGACATTCCTTGCAGAGTGGGGCTCTTTCAGTTGGCCGACAAAGAGGCC 410  
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361 CACCACCGGTGAACACATATCTCCACCGGGTGGCGGTGGCATCGTCTGCACCCCTGTGG 420  
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 421 GCCCTGCTCATCTCTGGGAAACAGTGTATCTTTTGTGGAGAACCATCTCTCTGCTGCAAGAG 480  
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 CD559652  
 CD559652.2 GI:38559024  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 731)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585720.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs@mail.nih.gov  
 Tissue procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: IRBK2 row: c column: 08  
 High quality sequence stop: 681.

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 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC



Frederick, MCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRAK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRAK.presv.dat) a Note: this is a NIH\_MGC Library."

## ORIGIN

```

Query Match      56.3%; Score 584.4; DB 14; Length 731;
Best Local Similarity 97.0%; Pred. No. 3.9e-146;
Matches 606; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 1 ATGTACACGGGTCTGCTGCGCATCGAGGGGGAACACCATCTCCAGGTGATCGCGCG 151
Db 92 ATGTACACGGGTCTGCTGCGCATCGAGGGGGAACACCATCTCCAGGTGATCGCGCG 151
QY 61 CTGCTCAATGTGGCTTGTGCTGGCGCACTAGGCAATGGGGTGGCGCTGTGTTTC 120
Db 152 CTGCTCAATGTGGCTTGTGCTGGCGCACTAGGCAATGGGGTGGCGCTGTGTTTC 120
QY 121 TGTCTCCACATGAAGACCTGGAGCCAGCAGCTGTTTACCTTTCAATTTGGCGGTGCT 180
Db 212 TGTCTCCACATGAAGACCTGGAGCCAGCAGCTGTTTACCTTTCAATTTGGCGGTGCT 180
QY 181 GATTTTCCTCTATCATCTGCTGCTTTCGGAAGAGCTATTAATCTTCAATTTGGCGGTGCT 271
Db 272 GATTTTCCTCTATCATCTGCTGCTTTCGGAAGAGCTATTAATCTTCAATTTGGCGGTGCT 271
QY 241 TGGGCTTTTGGGGACATTCCTCCGCGAGTGGGGCTTTCACGCTTGGCCATGAACAGGGCC 300
Db 332 TGGGCTTTTGGGGACATTCCTCCGCGAGTGGGGCTTTCACGCTTGGCCATGAACAGGGCC 300
QY 301 GGGAGCATCTGTTCTTACCGTGTGGCTGGGAGAGCTATTTCAAAAGTGGTCCACCCC 360
Db 392 GGGAGCATCTGTTCTTACCGTGTGGCTGGGAGAGCTATTTCAAAAGTGGTCCACCCC 360
QY 361 CACCAAGGGTGAACATCTATCCACCGGGTGGGGCTTTCGAGCATCTGCAACCTGTGG 420
Db 452 CACCAAGGGTGAACATCTATCTCCACCGGGTGGGGCTTTCGAGCATCTGCAACCTGTGG 420
QY 421 GCCCTGTCTATCTTGGGAACAGTGTATCTTTGCTGGAGAGCCATCTCTGGTGGAGAG 480
Db 512 GCCCTGTCTATCTTGGGAACAGTGTATCTTTGCTGGAGAGCCATCTCTGGTGGAGAG 480
QY 481 ACGGCGTCTCTGTGAGAGCTTTCATCATGGAGTGGGCAATGGCTGGCATGACATCATG 540
Db 572 ACGGCGTCTCTGTGAGAGCTTTCATCATGGAGTGGGCAATGGCTGGCATGACATCATG 540
QY 541 TTCCAGCTGGAGTTCCTTTATGCCCTTGGGATCATCTTATTTTGTCTCTTCAAGATTGT 600
Db 632 TTCCAGCTGGAGTTCCTTTATGCCCTTGGGATCATCTTATTTT--GCTCCTTCAGATTGT 689
QY 601 TGGAGCCTTGGAGGCGAGGCGAGCAGC 625
Db 690 TGGAGCTGANGCGGAGCAGAGCTGC 714

```

## RESULT 12

```

CD246157
LOCUS      1004 bp mRNA linear EST 22-MAY-2003
DEFINITION AGENCOURT 14127000 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6912801 5', mRNA sequence.
CD246157
VERSION    CD246157.1 GI:31006621
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS    1 (bases 1 to 1004)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.

```

Email: [cgapbs-@email.nih.gov](mailto:cgapbs-@email.nih.gov)  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRB101 row: e column: 08  
High quality sequence start: 106  
High quality sequence stop: 677.  
Location/Qualifiers  
1. .1004  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6912801"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XbaI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat) a Note: this is a NIH\_MGC Library."

## FEATURES

## source

## ORIGIN

```

Query Match      53.8%; Score 558.6; DB 14; Length 1004;
Best Local Similarity 99.3%; Pred. No. 4.2e-139;
Matches 561; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTCTGCTGCGCATCGAGGGGGAACACCATCTCCAGGTGATCGCGCG 60
Db 131 ATGTACACGGGTCTGCTGCGCATCGAGGGGGAACACCATCTCCAGGTGATCGCGCG 130
QY 61 CTGCTCAATGTGGCTTGTGCTGGCGGCACTAGGCAATGGGGTGGCGCTGTGTTTC 120
Db 191 CTGCTCAATGTGGCTTGTGCTGGCGGCACTAGGCAATGGGGTGGCGCTGTGTTTC 250
QY 121 TGCTTCCACATGAAGACCTGGAGCCAGCTGTTTACCTTTCAATTTGGCGGTGCT 180
Db 251 TGCTTCCACATGAAGACCTGGAGCCAGCTGTTTACCTTTCAATTTGGCGGTGCT 310
QY 181 GATTTCTCTCTATCATCTGCTGCTTTCGGAAGAGCTATTAATCTTCAATTTGGCGGTGCT 240
Db 311 GATTTCTCTCTATCATCTGCTGCTTTCGGAAGAGCTATTAATCTTCAATTTGGCGGTGCT 370
QY 241 TGGGCTTTTGGGGAATTCCTTGGAGTGGGGCTCTTTCAGCTTGGCCATGAACAGGGCC 300
Db 371 TGGGCTTTTGGGGAATTCCTTGGAGTGGGGCTCTTTCAGCTTGGCCATGAACAGGGCC 430
QY 301 GGGAGCATCTGTTCTTCTTGGAGTGGCTTGGAGAGCTATTTCAAAAGTGGTCCACCCC 360
Db 431 GGGAGCATCTGTTCTTCTTGGAGTGGCTTGGAGAGCTATTTCAAAAGTGGTCCACCCC 490
QY 361 CACCAAGGGTGAACATCTATCTCCACCGGGTGGGGCTGGCATGCTGCAACCTGTGG 420
Db 491 CACCAAGGGTGAACATCTATCTCCACCGGGTGGGGCTGGCATGCTGCAACCTGTGG 550
QY 421 GCCTGTGTCATCTGGGAACAGTGTATCTTTTGTGGAGAACCATCTCTCTGGTGCAGAG 480
Db 551 GCCTGTGTCATCTGGGAACAGTGTATCTTTTGTGGAGAACCATCTCTCTGGTGCAGAG 610
QY 481 ACGGCGTCTCTGTGAGAGCTTTCATCATGGAGTGGGCAATGGCTGGCATGACATCATG 540
Db 611 ACGGCGTCTCTGTGAGAGCTTTCATCATGGAGTGGGCAATGGCTGGCATGACATCATG 670
QY 541 TTCCAGCTGGAGTTCCTTTATGCCCTTGGGATCATCTTATTTT--GCTCCTTCAGATTGT 565

```



```

Db      671  TCCCACTGGAGTCTTTATACCCC 695

RESULT 13
LOCUS   CE432388/c
DEFINITION tigr-gss-dog-17000362997607 Dog Library Canis familiaris genomic,
ACCESSION CE432388
VERSION   CE432388.1 GI:367707139
KEYWORDS  GSS:
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris

REFERENCE
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
TITLE     The dog genome: survey sequencing and comparative analysis
JOURNAL   Science 301 (5641), 1898-1903 (2003)
MEDLINE   22875432
PUBMED    14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirkness@tigr.org
          Class: shotgun.
          Location/Qualifiers
            1..594
              /organism="Canis familiaris"
              /mol_type="genomic DNA"
              /strain="Standard Poodle"
              /db_xref="taxon:9615"
              /clone_lib="Dog Library"
              /note="Site 1: BstXI; Libraries were prepared from
              peripheral blood"

FEATURES
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         location(1..594)

ORIGIN
Query Match      43.7%; Score 453.8; DB 29; Length 594;
Best Local Similarity 85.3%; Pred. No. 5.8e-111;
Matches 506; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 376 ACTATCTCCACCGGTGGCGCTGGCATCTCTGCAACCTCTGTGGCCCTGGTATCTCTG 435
Db 594 ACCATTCCACCGGACTGGCATCTCTGCAACCTCTGTGGCCCTGGTATCTCTG 535
QY 436 GGACAGTGTATCTTTTCTGGAGAACCATCTCTGCGTGCAAGAGACGGCGTCTCTGT 495
Db 534 GGCACTCTCTACCTTTTGTATGGAGAACCATCTGCGTGCAAGAGACCATATCTTGT 475
QY 436 GAGAGCTTCATCATGGAGTGGCCAAATGGCTGGGATGACATCATGTTCCAGCTGGAGTTC 555
Db 474 GAGAGCTTCATCATGGAGTGGCCAAATGGCTGGGATGACATCATGTTCCAGCTGGAGTTC 415
QY 556 TTTATGCGCCCTCGGCATCATCTTATTTGCTCTCTTCAAGATGTTTGGAGCTGAGCGG 615
Db 414 TTCTCTCTCTGGGATCATCTCTGTTCTGCTCTCTGAGGATTTTGGAGTCTGAGCAG 355
QY 616 AGGAGAGCTGGCCAGACAGGCTCGGATGAAGAGCGACCCGGTTTCATCATGTTGGTG 675
Db 354 AGGCGGAGCTGGCCAGAGCTCGGATGAGAGAGCTACCGGTTTCATCATGTTGGTG 295
QY 676 GCAATTTGTTTCATCATGTTTACCTGCGAGCGTGTCTGTAGACTCTATTTCCTCTGG 735
Db 294 GCGGTTGTGTTTCATCATGTTTACCTGCGAGCGTGTCTGTAGACTCTATTTCCTCTGG 235
QY 736 ACCGTGCGCTCGAGTGTCTGCGATCCCTCTGTCCATGGGCGCCCTGACATACCTCAGC 795
Db 234 ACCGTGCGCTCGAGTGTCTGCGACCCCTCTGTCCAGTAGCCCTTCCACATCACCTCAGC 175

```

```

QY 796 TTCACCTACATGAACAGCATGCTGGATCCCTCGTGTATTATTTTCAAGCCCTCCTTT 855
Db 174 TTCACCTACATGAACAGCATGCTGGATCCCTCGTGTATTATTTTTCGAGTCTGTTATC 115
QY 856 CCCAATTCTACACAGCTCAAAATCTGAGTCTGAAACCCCAAGCAGCCAGGACTCA 915
Db 114 CCCAATTCTACACAGCTCAAGATCCGCGTTTTCGACCAAGAGTCCAGGCGACTCC 55
QY 916 AAAACACAAAGCCGGAAGAGATGCCAATTTCGAACCTCGTCCGAGGAGTTG 968
Db 54 AAGACCCAGAGCCCGGAAGAGATGCCAATCCCAAGCTCTGTCCAGAGTTG 2

RESULT 14
LOCUS   CB576966
DEFINITION AMGNNUC:URGP1-00001-C7-A urgp1 (14349) Rattus norvegicus cDNA clone
ACCESSION CB576966
VERSION   CB576966.1 GI:29521007
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus

REFERENCE
AUTHORS   Amgen EST Program.
TITLE     Amgen Rat EST Program
JOURNAL   Unpublished (2003)
COMMENT   Contact: Dan Fitzpatrick
          Amgen, Inc
          One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
          Tel: 805 447-4881
          Plate: 00001 row: c column: 7.
          Location/Qualifiers
            1..635
              /organism="Rattus norvegicus"
              /mol_type="mRNA"
              /db_xref="taxon:10116"
              /clone="urgp1-00001-c7"
              /clone_lib="urgp1 (14349)"
              /note="Vector: pSPORT1; Rat GPCR library rearrayed
              internal pSPORr vector"

FEATURES
         source
         location(1..635)

ORIGIN
Query Match      42.8%; Score 443.8; DB 14; Length 635;
Best Local Similarity 82.0%; Pred. No. 3e-108;
Matches 511; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 5 ACAACGGGTCTGTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCGTGC 64
Db 12 ACAACGGGTCTGTGCTCTCATCGAGGGGAAACCATCACCCAGGTATGCGCCTTTAC 71
QY 65 TCATTGTGGCTTTGTCTGCGCGCATAGGCATGGGCTCGCCCTGTGTGTCTGTCT 124
Db 72 TCATCTTGGCTCTCTCTCTGTGAGCCCTTGGCAACGGCTAGSCCTGTGTGTCTGTCT 131
QY 125 TCCACATGAAGACCTGGAAGCCAGCATGTTTACCTTTTCAATTTTGGCCGTGCTGATT 184
Db 132 TTACATGAGAGCTGAGAGCTGAGCACTATTACCTTTTCACTTTTGTGCTAGCCGATT 191
QY 185 TCCTCTTATGATCTGCTGCCCTTTTCGGACAGACTATTACCTCAGACGTAGACACTGGG 244
Db 192 TTCTCTCATGATCTGCTACCCCTTCGGACAGACTACTACCTCAGACGTAGGCACTTGA 251
QY 245 CTATTGGGACATCTCCCTGCGAGTGGGCTCTTCAGTTGGCCCATGAACAGGCGCGGA 304
Db 252 TTTTGGGGGATATTCCTCTGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 311
QY 305 GCATCTGTGTTCTCTAGCGTGGTGGCTGCGGACAGGTATTTCAAGTGGTCCACCCACC 364

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Db 312 GCATTGCTTCTCCTCAGTGTGGTGGCGGTGGACAGGATATTTCAAAGTGTCTCCACCCACC 371  
 Qy 365 ACGCGGTGAACACTATCTCCACCGGGTGGGGCTGGCATGCTGTGACACCTGTGGGCCC 424  
 Db 372 ATATGGTGAACGCCATCTCCAAATCGGACTGCGAGTGCCTGCTGTGCTCTCTGGAATT 431  
 Qy 425 TGGTCATCTGGGAACAGTGTATCTTTTGTCTGGAGAACCATCTCTGCTGCAAGAGAGCG 484  
 Db 432 TGGTCATCTGGGAGCTGTGTATCTTTGATGGAGAGTCACTGTGTGGGGGAGTGG 491  
 Qy 485 CCGTCTCTGTGAGAGCTTCATCATGGAGTGGCAATGGCTGGCATGACATCATGTTC 544  
 Db 492 TGTTCATCTGTGAGAGCTTCATCATGGAGTGGCAACCGGTGGCAACGATATCATGTTC 551  
 Qy 545 AGCTGGAGTTCTTTATGGCCCTCGGCATCATCTTATTTGTCTCTCAAGATTTGTTGA 604  
 Db 552 AGCTGGAGTTCTTCTGCGCCCTGACCATCATCTTGTCTGCTCTCAAAAGTGTGTTGA 611  
 Qy 605 GCCTGAGCGGAGGAGCAGCTG 627  
 Db 612 GCCTGAGACAGAGGCAACAGCTG 634

RESULT 15  
 BC027965  
 LOCUS BC027965 2146 bp mRNA linear HTC 01-MAY-2002  
 DEFINITION Homo sapiens, Similar to putative chemokine receptor; GTP-binding protein, clone IMAGE:5222688, mRNA.

ACCESSION BC027965  
 VERSION BC027965.1 GI:20379752  
 KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2146)

AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc.mgc@nhgri.nih.gov](mailto:nisc.mgc@nhgri.nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Laric, P., Legaspi, R., Maduro, Q. L.,

Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,

Pearson, R., Stantrispop, S., Thomas, P.D., Touchman, J.W., Teurgeon, C.,

Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A.,

Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IMAGE Plate: 49 Row: 1 Column: 24

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 5174460

This clone has the following problem: frame shifted.

Location/Qualifiers

1..2146

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

FEATURES

source

/clone="IMAGE:5222688"  
 /tissue type="Pancreas, Spleen, adult pooled"  
 /clone\_lib="NIH\_MGC\_120"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"

# ORIGIN

Query Match 35.7%; Score 370.8; DB 11; Length 2146;  
 Best Local Similarity 64.1%; Pred. No. 2.8e-88;  
 Matches 599; Conservative 0; Mismatches 317; Indels 18; Gaps 2;  
 Qy 1 ATGTACAAACGGGTCTGTCTGCGCATCGAGGGGGGACACCATCTCCACAGTGAATGGCGCG 60  
 Db 97 ATAGACAGAGAGAACTGCTGCTGTTCGAGATGACTTCATTGTCAAGGTGTGGCGCG 156  
 Qy 61 CTGCTCATTTGGCGCTTTTGTCTGGCGCACATGAGCAATGGGTGCGCTGTGTGGTTTC 120  
 Db 157 GTGTGGGGCTGGAGTTTATCTTCGGGGCTTCGGGCAATGGCCCTTGGCCCTTGGATTTTC 216  
 Qy 121 TGCTTCCACATGAGACCTGGAAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCGTGGCT 180  
 Db 217 TGTTCACCTCAAGTCTCGAAATCCAGCCGGATTTCTCTGTTCAACCTGAGATGGCT 276  
 Qy 181 GATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTACTCTCAGACTAGACAC 240  
 Db 277 GACTTTCTACTGATCATCTGCTGCTCTTCTCTGATGGAACAATATGTGAGGCGTTGGGAC 336  
 Qy 241 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGGCTTTCACGTTGGCCCATGACAGGGCC 300  
 Db 337 TGGAAATTTGGGGACATCCCTTGGCGGCTGATGCTCTTCATCTTGGCTATGAACCGCCAG 396  
 Qy 301 GGGAGCATGCTGTTTCTTACGGTGTGGCTGGGACAGGTATTTCAAAAGTGTGCCACCCC 360  
 Db 397 GGAGCATCATCTTCTCAGGTGTGGCGGTAGACAGGTATTTTCGGGTGTGTCATCCC 456  
 Qy 361 CACCAAGCGGTGAACACATCTATCTCCACCGGGTGGCGGTGGCATCTGTGCAACCCCTGTG 420  
 Db 457 CACCAGCCCTGAAACAAGATCTCCAATCGACAGAGCCATCATCTCTTGGCTTCTGTGG 516  
 Qy 421 GCCCTGTCTCCTGGGAAAGTGTATCTTTTGTCTGGAGAACCATCTCTGCTGCAAGAG 480  
 Db 517 GGCATCACTATTGGCTCGACAGTCCACCTCTCTGAAAGAGAGATGCCGATCAGAAATGC 576  
 Qy 481 ACGGCCGTCTCTGTGAGAGCTTCATCATGGAGTCCGCCAATGGTGGCATGACATCATG 540  
 Db 577 GGTGCAATTTGTGCGAGCTTCAGCATCTGCCATACCTCCAGTGGACAGAGCCATG 636  
 Qy 541 TTCCAGCTGGAGTTCTTTATGCCCCCTCGGCATCATCTTATTTTGTCTCTTCAAGATTGT 600  
 Db 637 TTCTCTCTGGAGTTCTTCTCTGCCCCCTGGGCATCATCTCTGCTCAGCCAGAAATATC 696  
 Qy 601 TGGAGCTTGGCGGAGGAGCGACGATGGCCAGAGGCTCGGATGAGAGGCGACCCCG 660  
 Db 697 TGGAGCTTGGCGGAGAG---ACAAATGAGACCGGCATGCCAAGATCAAGAGAGCCATCAC 753  
 Qy 661 TTCTATCATGTGTGGCAATTTGTGTTCATCATGTCTACCTCCAGCGCTGTCTGTCTAGA 720  
 Db 754 TTCTATCATGTGTGGCCATCTGTCTTCTCATCTCTGCTTCTTCCAGAGCTGTGTGGCG 813  
 Qy 721 CTCTATTTCTCTGAGAGGTTGCCCTC-----GAGTGCCTTGGCATCTCTCT 765  
 Db 814 ATCCGATCTTCTGGCTCTCTGCACACTTGGGACAGCAGAAATTTGTAAGTGTACCGCTCG 873  
 Qy 766 GTCCATGGGGCCCTGCACATACCTCTCAGCTTCAGTACATGAACAGCATCTGTCATCCC 825  
 Db 874 GTGGACCTGGGGTTCTTTTATCATCTCAGCTTCACCTACATGAACAGCATGTCGACCCC 933  
 Qy 826 CTGGTGTATTTTTCAGAGCCCTCTTTCACAAATTTCTACAAAGCTCAAAATCTGC 885  
 Db 934 GTGGGTACTACTTCTCTCAGGCCATCTTTCACAACTTCTTCCACTTTGATCAACCCG 993  
 Qy 886 AGTCTGAAACCAAGCAGCAGGACACTCAAAA 919

CC modulating cellular polypeptide expression or activity, useful as  
 CC antagonists and agonists in disease treatment  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 4; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGCFHMTWKPSVYLFNLAVA 60  
 DB 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGCFHMTWKPSVYLFNLAVA 60  
 QY 61 DFLMCLCPFRDYLYLRHWAFGDIPCRVGLFTLANNRAGSIVELTVVAADRYEKVVHP 120  
 DB 61 DFLMCLCPFRDYLYLRHWAFGDIPCRVGLFTLANNRAGSIVELTVVAADRYEKVVHP 120  
 QY 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 DB 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 QY 181 FOLEFFMPLGIILFCFSFKIWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR 240  
 DB 181 FOLEFFMPLGIILFCFSFKIWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR 240  
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTYMNWMLDPLVYFSSPSPKFNKIKISLKPX 300  
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTYMNWMLDPLVYFSSPSPKFNKIKISLKPX 300  
 QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
 DB 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 4  
 AAU06197  
 ID AAU06197 standard; protein; 346 AA.  
 AC AAU06197;  
 DT 19-DEC-2001 (first entry)  
 DE Novel human G protein-coupled receptor (GPCR) protein.  
 KW Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;  
 KW hyperproliferative disorder; neurological disorder; psychiatric disease;  
 KW inflammatory disorder; respiratory disorder.  
 XX  
 OS Homo sapiens.  
 PN WO200173029-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009522.  
 XX  
 PR 27-MAR-2000; 2000US-0192419P.  
 PR 06-SEP-2000; 2000US-0230459P.  
 PR 20-SEP-2000; 2000US-00666535.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Ye J, Cravchik A, Di Francesco V, Beasley EX;  
 XX  
 XX WPI; 2001-616503/71.  
 DR N-PSDB; AAS12581.  
 XX  
 PT Novel human G-protein coupled receptor proteins and nucleic acid  
 PT molecules encoding the protein for use in developing human therapeutics  
 PT and diagnostic compositions and for identifying modulators of the  
 PT protein.  
 XX  
 PS Claim 1; Fig 1; 66pp; English.

XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC coupled receptor (GPCR) which is related to the chemokine receptor  
 CC subfamily. The cDNA and gene sequences encoding for GPCR are also given  
 CC in the invention. The sequences of the invention are useful for  
 CC diagnosing and treating diseases or conditions mediated by human  
 CC proteases. Such diseases include hyperproliferative disorders (e.g.  
 CC hyperplasia), neurological disorders (e.g. Parkinson's disease),  
 CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g.  
 CC diabetes), and respiratory disorders (e.g. adult respiratory distress  
 CC syndrome, ARDS). The GPCR protein is also useful for identifying a  
 CC modulator of the expression of the protein. It also serves as a target  
 CC for identifying agents for use in mammalian therapeutic applications,  
 CC e.g. a human drug, particularly modulating a biological or pathological  
 CC response in a cell or tissue that expresses the protein, in biological  
 CC assays related to GPCRs that are related to members of the chemokine  
 CC receptor subfamily, in drug screening assays and in competition binding  
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to  
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The  
 CC polynucleotide sequences can also be used in gene therapy. The present  
 CC sequence represents the novel human GPCR of the invention.  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 4; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGCFHMTWKPSVYLFNLAVA 60  
 DB 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGCFHMTWKPSVYLFNLAVA 60  
 QY 61 DFLMCLCPFRDYLYLRHWAFGDIPCRVGLFTLANNRAGSIVELTVVAADRYEKVVHP 120  
 DB 61 DFLMCLCPFRDYLYLRHWAFGDIPCRVGLFTLANNRAGSIVELTVVAADRYEKVVHP 120  
 QY 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 DB 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 QY 181 FOLEFFMPLGIILFCFSFKIWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR 240  
 DB 181 FOLEFFMPLGIILFCFSFKIWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR 240  
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTYMNWMLDPLVYFSSPSPKFNKIKISLKPX 300  
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTYMNWMLDPLVYFSSPSPKFNKIKISLKPX 300  
 QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
 DB 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 4  
 AAU04373  
 ID AAU04373 standard; protein; 346 AA.  
 AC AAU04373;  
 DT 23-OCT-2001 (first entry)  
 DE Human G-protein coupled receptor, hrup19.  
 XX  
 XX Human; G-protein coupled receptor; GPCR; hrup19; agonist;  
 KW inverse agonist; lung cancer.  
 XX  
 OS Homo sapiens.  
 PN WO200136471-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 16-NOV-2000; 2000WO-US031509.

XX	17-NOV-1999;	99US-0160088P.
PR	17-NOV-1999;	99US-0166099P.
PR	17-NOV-1999;	99US-0166369P.
PR	23-DEC-1999;	99US-0171900P.
PR	23-DEC-1999;	99US-0171901P.
PR	23-DEC-1999;	99US-0171902P.
PR	11-FEB-2000;	2000US-0181749P.
PR	14-MAR-2000;	2000US-0189258P.
PR	14-MAR-2000;	2000US-0189259P.
PR	10-APR-2000;	2000US-0195898P.
PR	10-APR-2000;	2000US-0195899P.
PR	10-APR-2000;	2000US-0196078P.
PR	28-APR-2000;	2000US-0200419P.
PR	13-MAY-2000;	2000US-0203630P.
PR	12-JUN-2000;	2000US-0210714P.
PR	12-JUN-2000;	2000US-0210582P.
PR	21-AUG-2000;	2000US-0226760P.
PR	26-SEP-2000;	2000US-0235418P.
PR	26-SEP-2000;	2000US-0235779P.
PR	20-OCT-2000;	2000US-0242332P.
PR	20-OCT-2000;	2000US-0242343P.
PR	24-OCT-2000;	2000US-0243019P.
XX		
PA	(AREN-) ARENA PHARM INC.	
XX		
PI	Chen R, Dang HT, Lowitz KP,	
XX	WPI; 2001-355616/37.	
DR	N-PSDB; AAS07946.	

Qy	301	QPGHSKTQRDEMPISNLGRRCISIVANSFQSQSDGQWDPIVEMH 346
Db	301	QPGHSKTQRDEMPISNLGRRCISIVANSFQSQSDGQWDPIVEMH 346
RESULT 5		
AAAE16172		
ID	AAE16172	standard; protein, 346 AA.
XX		
AC	AAE16172;	
XX		
DT	26-MAR-2002	(first entry)
XX		
DE	Human G-protein coupled receptor 3 (GCRG-3) protein.	
XX		
KW	Human; G-protein coupled receptor 3; cell proliferative disorder; arteriosclerosis; hepatitis; cancer; neurological disorder; Alzheimer's disease; Parkinson's disease; cardiovascular disease; atherosclerosis; hypertension; myocardial infarction; peptic gastrointestinal disorder; dysphagia; anorexia; autoimmune acquired immune deficiency syndrome; inflammatory disorder; Addison's disease; allergy; Grave's disease; metabolic disorders; diabetes; obesity; osteoporosis; gene therapy; GCRG-3.	
XX		
OS	Homo sapiens.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..32
FT		/label= Signal_peptide
FT	Domain	20..44
FT		/note= "Transmembrane domain"
FT	Protein	33..346
FT		/label= Human_mature_GCRG-3_protein
FT	Domain	93..110
FT		/note= "Transmembrane domain"
FT	Domain	137..154
FT		/note= "Transmembrane domain"
FT	Domain	222..244
FT		/note= "Transmembrane domain"
XX		
PN	WO200107937-A2.	
XX		
XX		
PD	22-NOV-2001.	
XX		
PF	17-MAY-2001; 2001WO-US016285.	
XX		
XX	18-MAY-2000; 2000US-0205628P.	
PR	22-MAY-2000; 2000US-0206222P.	
PR	25-MAY-2000; 2000US-0207566P.	
PR	02-JUN-2000; 2000US-020834P.	
PR	02-JUN-2000; 2000US-0208661P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
PI	Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, G	
PI	Khan PA, Gandhi AR, Walla NK, Nguyen DB, Yue H, Hafalil	
PI	Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Yo	
XX		
DR	WPI; 2002-089844/12.	
DR	N-PSDB; AAD26371.	
XX		
XX		
PT	Novel G-protein coupled receptors and polynucleotides useful	
PT	diagnosis, treatment and prevention of disorders of cell pr	
PT	neurological, cardiovascular, metabolic disorders and viral	
XX		
PS	Claim 1; Page 105-106; 115pp; English.	
XX		
CC	The invention relates to human G-protein coupled receptor (	
CC	polypeptides and polynucleotides. GCRG polypeptides are us	
CC	screening compounds that modulate their activity. They are	
CC	diagnosis, prevention and treatment of disorders which incl	
CC	proliferative disorders such as arteriosclerosis, hepatitis	







AC ABB08596;  
 XX 01-JUL-2002 (first entry)  
 XX Human lipocyte-originated G protein-coupled receptor protein TGR13.  
 DE Antiinflammatory; anorectic; obesity; inflammation; gene therapy; human;  
 XX G protein-coupled receptor protein TGR13.  
 XX Homo sapiens.  
 XX WO200202767-A1.  
 XX 10-JAN-2002.  
 XX 02-JUL-2001; 2001WO-JP005711.  
 XX 04-JUL-2000; 2000JP-00206860.  
 XX 31-JUL-2000; 2000JP-00235274.  
 XX (TAKE ) TAKEEDA CHEM IND LTD.  
 XX PA  
 XX PI Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;  
 XX WPI; 2002-164535/21.  
 XX N-PSDB; ABA99236.  
 XX New human lipocyte-originated G protein-coupled receptor proteins TGR13  
 PT and encoding DNAs, for developing drugs to treat obesity and  
 PT inflammations, including gene therapy.  
 XX Claim 1; Fig 2; 101pp; Japanese.  
 XX This invention relates to a human lipocyte-originated G protein-coupled  
 CC receptor proteins TGR13, thought to be antiinflammatory and anorectic in  
 CC their action. The proteins and encoded DNAs are for use in developing  
 CC drugs to treat obesity and inflammation, including gene therapy. The  
 CC present sequence represents the human lipocyte-originated G protein-  
 CC coupled receptor protein TGR13  
 XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYNGSCCRIBGDTISQVMPPLIIIVAFVLGALNGVALCGFCFHKMTWKBPSTVYLFNLAVA 60  
 DB 1 MYNGSCCRIBGDTISQVMPPLIIIVAFVLGALNGVALCGFCFHKMTWKBPSTVYLFNLAVA 60  
 QY 61 DELLMLICLPRTDYLLRRRWATGDI PCRVGLFTLANRAGSI VFLTVVAADRYFKVHP 120  
 DB 61 DELLMLICLPRTDYLLRRRWATGDI PCRVGLFTLANRAGSI VFLTVVAADRYFKVHP 120  
 QY 121 HVAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 DB 121 HVAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 QY 181 FOLEPFMPLGILFCFSKIVLSLRRRQQLARQARMKKATRFIMVAIVTTCVLPVSAR 240  
 DB 181 FOLEPFMPLGILFCFSKIVLSLRRRQQLARQARMKKATRFIMVAIVTTCVLPVSAR 240  
 QY 241 LYFLWTVPSSACDPSVHGALHITLSTYTNKMSMLDPLVYFSSPSPKFKYKLCISLKP 300  
 DB 241 LYFLWTVPSSACDPSVHGALHITLSTYTNKMSMLDPLVYFSSPSPKFKYKLCISLKP 300  
 QY 301 QFGHKTQPEEMPIISNLGRRCISVANSFQSDGQWDPHIVEMH 346  
 DB 301 QFGHKTQPEEMPIISNLGRRCISVANSFQSDGQWDPHIVEMH 346

RESULT 9  
 ABG93786

ID ABG93786 standard; protein; 346 AA.  
 XX AC ABG93786;  
 XX DT 26-NOV-2002 (first entry)  
 XX DE Human G protein-coupled receptor protein, nGPCR-11.  
 XX KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;  
 KW nG protein coupled receptor; communication; serpentine structure;  
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;  
 KW genetic predisposition; brain; immune response; gene therapy;  
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;  
 KW Huntington's disease; dyskinesia; manic depression; stroke;  
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;  
 XX KW tranquiliser.  
 XX OS Homo sapiens.  
 XX PN WO200264789-A1.  
 XX XX 22-AUG-2002.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX 14-FEB-2001; 2001WO-US004641.  
 XX PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX PI Lind P, Parodi LA, Vogeli G, Wood LS;  
 XX WPI; 2002-674879/72.  
 XX N-PSDB; ABS70241.  
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,  
 PT useful for treating or diagnosing a mental disorder or a disorder  
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or  
 PT Parkinson's disease.  
 XX Example 1; Page 84; 244pp; English.  
 XX The invention discloses an isolated human polypeptide, and encoding  
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the  
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the  
 CC communication between cells and their environment and are characterised  
 CC by a serpentine structure that passes through the cell membrane seven  
 CC times, hence the reason such receptors are sometimes called seven  
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are  
 CC useful for identifying an nGPCR allelic variant that correlates with a  
 CC mental disorder, for isolating an antibody that binds to an epitope of  
 CC the polypeptide, for identifying a compound that binds to a polypeptide or  
 CC polynucleotide and/or modulates its biological activity, for screening a  
 CC human subject to diagnose a disorder, or a genetic predisposition to a  
 CC disorder, affecting the brain or a genetic predisposition to a disorder,  
 CC for identifying compounds useful for the treatment of a mental disorder,  
 CC and for identifying a compound useful as a modulator of binding between  
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also  
 CC useful for inducing an immune response in a mammal. The nucleic acid or  
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.  
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,  
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's  
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also  
 CC be used for treating diabetes, inflammation or wounds. The sequences  
 CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR  
 CC referred to as beGPCRs) proteins  
 XX Sequence 346 AA;  
 SQ

Query Match 100.0%; Score 1853; DB 5; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIBGDTISQVMPPLIIIVAFVLGALNGVALCGFCFHKMTWKBPSTVYLFNLAVA 60

Db 1 MYNGSCCRLEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKSTVYLENLAVA 60  
QY 61 DFLLMICLPFRDYLYLRRRHAFGDI PCRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120  
Db 61 DFLLMICLPFRDYLYLRRRHAFGDI PCRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120  
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
QY 181 FOLEFFMPLGIILFCSEFKIVMSLRROQLARQARMKATRFIMVVAIVITCYLPSVSAR 240  
Db 181 FOLEFFMPLGIILFCSEFKIVMSLRROQLARQARMKATRFIMVVAIVITCYLPSVSAR 240  
QY 241 LYFLWTVPSSACDPSVHGALHTLSTFTYVNSMLDPLVYFSSPSPKFYNKIKICSLKPK 300  
Db 241 LYFLWTVPSSACDPSVHGALHTLSTFTYVNSMLDPLVYFSSPSPKFYNKIKICSLKPK 300  
QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
Db 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 10  
ABP95599  
ID ABP95599 standard; protein; 346 AA.

XX AC ABP95599;

XX DT 06-MAR-2003 (first entry)

XX DE Human GPCR polypeptide SEQ ID NO 8.

XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
KW drug development; gustatory; taste; fragrance; receptor.

XX OS Homo sapiens.

XX EN WO200216548-A2.

XX PD 28-FEB-2002.

XX PF 30-JUL-2001; 2001WO-IB0001446.

XX PR 04-AUG-2000; 2000JP-00237818.

XX PR 13-FEB-2001; 2001JP-00034434.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Haga T, Takeda S, Mitaku S;

XX DR WEI; 2002-304118/34.

XX DR N-PSDB; ABZ42873.

XX Database global search for G protein-coupled receptors, proteins and  
PT encoded genes for studying in vivo signal transduction mechanism and  
PT identifying targets for drug development.

XX PS Claim 10; SEQ ID NO 8; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled  
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-  
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane  
CC domains with 250-1000 amino acid residues to give a gene homologous with  
CC a known GPCR gene. The receptor proteins and encoded genes are useful for  
CC studying in vivo signal transduction mechanism and identifying targets  
CC for drug development e.g. based on olfactory and gustatory receptors in  
CC form of agonists and antagonists by screening intrinsic and extrinsic  
CC ligands as bitter taste inhibitors, taste enhancers and fragrance  
CC improvers. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX SQ Sequence 346 AA;  
Query Match 100.0%; Score 1853; DB 5; Length 346;  
Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYNGSCCRLEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKSTVYLENLAVA 60  
Db 1 MYNGSCCRLEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKSTVYLENLAVA 60  
QY 61 DFLLMICLPFRDYLYLRRRHAFGDI PCRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120  
Db 61 DFLLMICLPFRDYLYLRRRHAFGDI PCRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120  
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLENHLCVQETAVSCSFIMESANGWHDIM 180  
QY 181 FOLEFFMPLGIILFCSEFKIVMSLRROQLARQARMKATRFIMVVAIVITCYLPSVSAR 240  
Db 181 FOLEFFMPLGIILFCSEFKIVMSLRROQLARQARMKATRFIMVVAIVITCYLPSVSAR 240  
QY 241 LYFLWTVPSSACDPSVHGALHTLSTFTYVNSMLDPLVYFSSPSPKFYNKIKICSLKPK 300  
Db 241 LYFLWTVPSSACDPSVHGALHTLSTFTYVNSMLDPLVYFSSPSPKFYNKIKICSLKPK 300  
QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
Db 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 11

AAO14788

ID AAO14788 standard; protein; 346 AA.

XX AC AAO14788;

XX DT 28-JUN-2002 (first entry)

XX DE Human purinergic-like G-protein coupled receptor (AXOR87).

XX KW Human; purinergic-like G-protein coupled receptor; AXOR87; immunity;  
KW autoimmunity; inflammation; immunodeficiency; bacterial infection;  
KW fungal infection; viral infection; protozoa infection; cancer; diabetes;  
KW obesity; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;  
KW osteoarthritis; psychotic disorder; neurological disorder; vaccine;  
KW chromosome 12q24.

XX OS Homo sapiens.

XX OS GB2365868-A.

XX PD 27-FEB-2002.

XX PF 25-MAY-2001; 2001GB-00012860.

XX PR 30-MAY-2000; 2000US-00580675.

XX PR 02-NOV-2000; 2000GB-00026839.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX (GLAX ) GLAXO GROUP LTD.

XX Ignar DM, Elshourbagy N, Gattu M, Shabon U;

XX WEI; 2002-364852/40.

XX DR N-PSDB; AAL42499.

XX New purinergic-like G-protein coupled receptor AXOR87 polypeptide and  
PT polynucleotide, useful for treating diseases related to autoimmunity,  
PT inflammation, immunodeficiency, or bacterial, fungal, viral and protozoal  
PT infections.

XX Claim 2; Page 36; 47pp; English.

XX The invention comprises the amino acid and coding sequence of the human

CC purine-like G-protein coupled receptor AXOR87. The AXOR87 DNA and

CC protein sequences of the invention may be used for treating diseases

CC related to immunity, autoimmunity, inflammation, immunodeficiency, and

CC infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and

CC protein sequences are particularly useful for treating: cancers,

CC diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid

CC arthritis, osteoarthritis, as well as psychotic and neurological

CC disorders. The AXOR87 DNA and protein sequences may also be used as

CC vaccines. The present amino acid sequence (encoded by a sequence located

CC on chromosome 12q24) represents the human AXOR87 protein

XX

SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;

Best Local Similarity 100.0%; Pred. No. 5.9e-199;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLIVAFVLGALGVGVALCGCFHMKTKKSTVYLENLAVA 60

Db |||||||

QY 1 MYNGSCCRIEGDTISQVMPPLIVAFVLGALGVGVALCGCFHMKTKKSTVYLENLAVA 60

Db |||||||

QY 61 DFLMICLPFTDYLLRRHWAFGDIPCRVGLFTLAMNAGSIVFTVVAADRYFAKVHP 120

Db |||||||

QY 61 DFLMICLPFTDYLLRRHWAFGDIPCRVGLFTLAMNAGSIVFTVVAADRYFAKVHP 120

Db |||||||

QY 121 HVAVNTISTRVAAGIVCTLWALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIM 180

Db |||||||

QY 121 HVAVNTISTRVAAGIVCTLWALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIM 180

Db |||||||

QY 181 FQLEFFMPLGILLFCSEKIVLSRRQOLARQAKKATRFIMVAIVPITCILPSVSAR 240

Db |||||||

QY 181 FQLEFFMPLGILLFCSEKIVLSRRQOLARQAKKATRFIMVAIVPITCILPSVSAR 240

Db |||||||

QY 241 LYFTWTPSSACDPVSHGALHITLSFTYNNMMLDPLVYFSSPPKFKYKIKICSLPK 300

Db |||||||

QY 241 LYFTWTPSSACDPVSHGALHITLSFTYNNMMLDPLVYFSSPPKFKYKIKICSLPK 300

Db |||||||

QY 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346

Db |||||||

QY 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346

Db |||||||

RESULT 12

AAE24354

ID AAE24354 standard; protein; 346 AA.

XX

AC AAE24354;

XX

DT 04-OCT-2002 (first entry)

XX

DE Human G protein coupled receptor (GPCR), 57242 protein.

XX

KW Human; G protein coupled receptor; GPCR; 57242 protein; overweight;

KW metabolic disorder; lipogenesis; lipolysis; immunomodulator; heart;

KW bone disorder; osteoporosis; osteogenesis; bone resorption; cachexia;

KW hyperlipidaemia; anorexia; haematopoietic disorder; osteopathic;

KW autoimmune disorder; psoriasis; multiple sclerosis; brain disorder;

KW degenerative disease; Alzheimer's disease; Pick disease; diabetes;

KW adipocyte; hyperplastic growth; hypertrophic growth; gene therapy;

KW obesity; anorectic; receptor.

XX

OS Homo sapiens.

XX

PH Location/Qualifiers

FT Peptide 1..37

FT /label= Signal\_peptide

FT Domain 1..20

FT /note= "N-terminal non-transmembrane domain"

FT Modified-site 3..6

FT Cleavage-site

FT 9..10 /note= "N-glycosylation site"

FT 21..42 /note= "Cleavage site for mitochondrial preseq"

FT 32..278 /note= "Transmembrane domain"

FT 38..346 /note= "GPCR domain"

FT 43..51 /note= "Human mature GPCR protein"

FT 52..70 /note= "Non-transmembrane domain"

FT 71..89 /note= "Transmembrane domain"

FT 77..80 /note= "Extracellular loop"

FT 90..111 /note= "Nuclear localisation signal"

FT 112..130 /note= "Transmembrane domain"

FT 131..152 /note= "Non-transmembrane domain"

FT 153..184 /note= "Transmembrane domain"

FT 185..201 /note= "Extracellular loop"

FT 202..220 /note= "Transmembrane domain"

FT 204..220 /note= "Non-transmembrane domain"

FT 216..219 /note= "Nuclear localisation signal"

FT 221..245 /note= "CAMP- and CGMP-dependent protein kinase phosphorylation site"

FT 245..258 /note= "Transmembrane domain"

FT 246..255 /note= "Extracellular loop"

FT 259..280 /note= "Non-transmembrane domain"

FT 281..346 /note= "Transmembrane domain"

FT /note= "C-terminal cytoplasmic domain"

XX WO200218579-A2.

XX 07-MAR-2002.

XX 29-AUG-2001; 2001WO-US026882.

XX 29-AUG-2000; 2000US-0228409P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA;

XX MPI; 2002-479433/51.

XX N-PSDR; AAD39181.

XX Human G protein coupled receptor nucleic acid and polypeptide molecules,

XX designated 57242, useful for diagnosing, preventing or treating aberrant

XX lipogenesis or aberrant lipolysis, obesity, diabetes or bone disorders

XX (e.g. osteoporosis).

XX Claim 9; Page 112-113; 114pp; English.

XX The invention relates to G protein coupled receptor (GPCR) family member,

XX 57242 and its corresponding nucleic acid sequence. The 57242 nucleic acid

XX and polypeptide are useful for diagnosing, preventing or treating a

XX subject having or at risk of developing a metabolic disorder,

XX particularly a disorder associated with aberrant lipogenesis or aberrant

XX lipolysis, obesity or diabetes. The 57242 DNA and protein are also useful

CC for treating a subject having bone disorder, where the disorder is  
 CC osteoporosis or a disorder associated with aberrant osteogenesis or  
 CC aberrant bone resorption. These diseases include obesity, diabetes,  
 CC hyperlipidaemia, overweight, anorexia or cachexia. The 57242 DNA and  
 CC protein are also useful for treating a subject having haematopoietic  
 CC disorders, autoimmune disorders e.g. psoriasis and multiple sclerosis,  
 CC brain disorders, degenerative diseases e.g. Alzheimer's disease and Pick  
 CC disease and disorders involving heart. The 57242 nucleic acid and  
 CC polypeptide are also useful for modulating adipocyte activity such as  
 CC hyperplastic growth, hypertrophic growth or lipogenesis. The 57242 DNA is  
 CC used in gene therapy. The present sequence is human 57242 protein  
 XX  
 XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60  
 DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60  
 QY 61 DFLMICLPFTDYLLRRRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120  
 DB 61 DFLMICLPFTDYLLRRRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120  
 QY 121 HAVNTISTRVAAGIVCTLWALVILGTVLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 DB 121 HAVNTISTRVAAGIVCTLWALVILGTVLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 QY 181 FOLEFMPPLGILFCSEFKIVSLRRRQOLARQARMKATRFIMVAIVFITCYLPSVSAR 240  
 DB 181 FOLEFMPPLGILFCSEFKIVSLRRRQOLARQARMKATRFIMVAIVFITCYLPSVSAR 240  
 QY 241 LYFLWTVPSACDPSVHGALHITLSFTYNNMLDPLVYFESSSPFPKYNKLCISLKP 300  
 DB 241 LYFLWTVPSACDPSVHGALHITLSFTYNNMLDPLVYFESSSPFPKYNKLCISLKP 300  
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

## RESULT 13

ABP81747  
 ID ABP81747 standard; protein; 346 AA.

XX AC ABP81747;

XX 04-MAR-2003 (first entry)

DE Human chemokine receptor FKSG80/GPR81 protein SEQ ID NO:668.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.

XX Homo sapiens.

OS WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; AB242592.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related diseases, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242969 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 6; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60  
 DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60  
 QY 61 DFLMICLPFTDYLLRRRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120  
 DB 61 DFLMICLPFTDYLLRRRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120  
 QY 121 HAVNTISTRVAAGIVCTLWALVILGTVLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 DB 121 HAVNTISTRVAAGIVCTLWALVILGTVLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 QY 181 FOLEFMPPLGILFCSEFKIVSLRRRQOLARQARMKATRFIMVAIVFITCYLPSVSAR 240  
 DB 181 FOLEFMPPLGILFCSEFKIVSLRRRQOLARQARMKATRFIMVAIVFITCYLPSVSAR 240  
 QY 241 LYFLWTVPSACDPSVHGALHITLSFTYNNMLDPLVYFESSSPFPKYNKLCISLKP 300  
 DB 241 LYFLWTVPSACDPSVHGALHITLSFTYNNMLDPLVYFESSSPFPKYNKLCISLKP 300  
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346  
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 14  
 ABP56751  
 ID ABP56751 standard; protein; 346 AA.  
 XX  
 AC ABP56751;  
 XX  
 DT 31-MAR-2003 (first entry)  
 XX  
 DE Human GAVE3 protein SEQ ID NO:2.  
 XX  
 DE Human; GAVE3; G protein-coupled receptor; GPCR; antiinflammatory;  
 KW antiasthmatic; antirheumatic; antiarthritic; inflammatory disorder;  
 KW asthma; chronic obstructive pulmonary disease; rheumatoid arthritis;  
 KW chromosome 12.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003000846-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019490.  
 XX  
 PR 22-JUN-2001; 2001US-00886041.  
 XX  
 PA (AVET) AVENTIS PHARM INC.  
 XX  
 PI Xia T, Ni D, Bishindrello H, Ardati A, Minnich A, Jupp R;  
 XX  
 DR WPI; 2003-184040/18.  
 DR N-PSDB; AB222648.  
 XX  
 PT New GAVE3 nucleic acid and polypeptide, for preventing or treating a  
 PT disorder associated with aberrant GAVE3 expression or activity, e.g.  
 PT inflammatory disease, asthma, chronic obstructive pulmonary disease or  
 PT rheumatoid arthritis.  
 XX  
 PS Claim 9; Fig 2; 90pp; English.  
 XX  
 CC The present sequence represents a human G protein-coupled receptor  
 CC (GPCR), designated GAVE3. GAVE3 is located on human chromosome 12. GAVE3  
 CC has antiinflammatory, antiasthmatic, antirheumatic and antiarthritic  
 CC activities. GAVE3 nucleic acids, polypeptides, agonists and antagonists  
 CC can be used for preventing or treating a disorder associated with  
 CC aberrant GAVE3 expression or activity, e.g. inflammatory disorders such  
 CC as asthma, chronic obstructive pulmonary disease or rheumatoid arthritis.  
 CC The nucleic acids and polypeptides can also be useful for identifying  
 CC modulators, i.e. candidate or test compounds, that bind to GAVE3 proteins  
 CC or have a stimulatory or inhibitory effect on GAVE3 expression or  
 CC activity. The nucleotide sequences can also be used for chromosomal  
 CC mapping, tissue typing or forensic biology. Host cells comprising GAVE3  
 CC can be used for producing non-human transgenic animals for studying the  
 CC function and/or activity of GAVE3, or for identifying and/or evaluating  
 CC modulators of GAVE3 activity  
 XX  
 SQ Sequence 346 AA;  
 Query Match 100.0%; Score 1853; DB 6; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYNGSCCRIGEDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKTKWKPSTVYLFNLAVA 60  
 Db 1 MYNGSCCRIGEDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKTKWKPSTVYLFNLAVA 60  
 QY 61 DFLIMICLPRTDYLLRRHWAFGDIPCRVGLFTLANRAGSIVFLTVAAADRYFKVWHP 120  
 Db 61 DFLIMICLPRTDYLLRRHWAFGDIPCRVGLFTLANRAGSIVFLTVAAADRYFKVWHP 120  
 QY 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180  
 Db 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

RESULT 15  
 AAO26511  
 ID AAO26511 standard; protein; 346 AA.  
 XX  
 AC AAO26511;  
 XX  
 DT 13-FEB-2003 (first entry)  
 XX  
 DE Human G-Protein Coupled Receptor protein.  
 XX  
 KW Anorectic; antidiabetic; antilipaeamic; antiasthmatic; antiinflammatory;  
 KW antiallergic; antianginal; nephrotropic; hepatotropic; immunosuppressive;  
 KW virucide; G-Protein-agonist; G-Protein-antagonist; dyslipidaemia; GPCR;  
 KW G-Protein Coupled Receptor; obesity; diabetes; asthma; bronchitis;  
 KW allergy; angina; glomerulonephritis; hepatitis; allograft rejection;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200283736-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 14-FEB-2002; 2002WO-US004397.  
 XX  
 PR 14-FEB-2001; 2001US-0269040P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Elliott SG, Rogers N, Busse LA;  
 XX  
 DR WPI; 2003-075524/07.  
 DR N-PSDB; AAU53846.  
 XX  
 PT New GPCR polypeptide and encoding nucleic acid molecule, useful for  
 PT diagnosis, treatment and/or prevention of diseases associated with GPCR  
 PT polypeptides, such as obesity, diabetes, asthma, allergies, angina and  
 PT hepatitis.  
 XX  
 PS Claim 13; Fig 1; 122pp; English.  
 XX  
 CC The invention relates to a novel isolated G-Protein Coupled Receptor  
 CC (GPCR) protein. The methods and compositions of the present invention are  
 CC useful for diagnosis, treatment, amelioration and/or prevention of  
 CC diseases associated with G-Protein Coupled Receptor (GPCR) polypeptides,  
 CC such as obesity, diabetes, dyslipidaemia, asthma, bronchitis, allergies,  
 CC angina, glomerulonephritis, hepatitis and allograft rejection. This  
 CC sequence represents the human GPCR protein of the invention  
 XX  
 SQ Sequence 346 AA;  
 Query Match 100.0%; Score 1853; DB 6; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-199;  
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYNGSCCRIGEDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKTKWKPSTVYLFNLAVA 60  
 Db 1 MYNGSCCRIGEDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKTKWKPSTVYLFNLAVA 60  
 QY 61 DFLIMICLPRTDYLLRRHWAFGDIPCRVGLFTLANRAGSIVFLTVAAADRYFKVWHP 120

Db 994 TGCCTCCAGAGGAGGATGACAGGTGAGCCAGATA 1027

Search completed: July 3, 2004, 08:42:48  
Job time : 3254 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2004, 07:48:36 ; Search time 559 Seconds  
(without alignments)  
8958.010 Million cell updates/sec

**Title:** US-10-076-260-1

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Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

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Maximum Match 100%

Database :

Database : Published Applications NA:\*

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19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	100.0	1038	15	US-10-240-842-1
2	1038	100.0	1038	15	US-10-076-260-1
3	1038	100.0	1038	17	US-10-332-032-2
4	1038	100.0	1041	9	US-09-862-274-1
5	1038	100.0	1041	9	US-09-886-041-1
6	1038	100.0	1041	10	US-09-782-374C-79
7	1038	100.0	1041	13	US-10-343-650A-7
8	1038	100.0	1041	15	US-10-188-149A-1
9	1038	100.0	1041	15	US-10-079-384-17
10	1038	100.0	1041	15	US-10-321-807-23
11	1038	100.0	1050	13	US-10-210-172-177
12	1038	100.0	1050	15	US-10-044-643-1
13	1038	100.0	1050	15	US-10-044-643-3
14	1038	100.0	1057	13	US-10-210-172-183
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					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 79, Appli
					Sequence 7, Appli
					Sequence 1, Appli
					Sequence 17, Appli
					Sequence 23, Appli
					Sequence 177, App
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 183, App

## ALIGNMENTS

## RESULT 1

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US-10-240-842-1
; Sequence 1, Application US/10240842
; Publication NO. US20030109673A1
; GENERAL INFORMATION:
; APPLICANT: xiao, yonghong
; TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974. 00883
; CURRENT APPLICATION NUMBER: US/10/240, 842
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/194, 701
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-240-842-1

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	Query Match	100.0%;	Score 1038;	DB 15;	Length 1038;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1038;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTACAA	CGGTCGTGCTGCGCGCATCGAGGGGGACACATCTCCACGATGATGCCGCG	60	
Db	1	ATGTACAA	CGGTCGTGCTGCGCGCATCGAGGGGGACACATCTCCACGATGATGCCGCG	60	
QY	61	CTGCTCAT	TGNGCCTTTTGTCGGGCGCACTAGGCAATGGGGTGCCTCTGTGTGGTTTC	120	
Db	61	CTGCTCAT	TGNGCCTTTTGTCGGGCGCACTAGGCAATGGGGTGCCTCTGTGTGGTTTC	120	
QY	121	TGCTTCCAC	TGAAGCACTGAGGCCGACACTGTTTACCTTTTCAATTTGGCCGTGGCT	180	
Db	121	TGCTTCCAC	TGAAGCACTGAGGCCGACACTGTTTACCTTTTCAATTTGGCCGTGGCT	180	
QY	181	GATTTCCCT	CCTTATGATCTGCTCGCTTTTCGGACAGACTATTACTCAGACGTAGACAC	240	

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Db 181 GATTTCCTCTTATGATGCTGCTGCTTTTGGACAGACTATTACCTCAGAGCTAGAC 240
Qy 241 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTCTTCAAGTGGCCATGACAGGGCC 300
Db 241 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTCTTCAAGTGGCCATGACAGGGCC 300
Qy 301 GGGAGCTGCTGCTTCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360
Db 301 GGGAGCTGCTGCTTCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360
Qy 361 CACACGGGCTGAAACATATCTCCACCGGGTGGGCTGGCATCGTCTGCACCTGTGG 420
Db 361 CACACGGGCTGAAACATATCTCCACCGGGTGGGCTGGCATCGTCTGCACCTGTGG 420
Qy 421 GCGCTGGTCACTCCCTGGGACAGTGTATCTTTGCTGGGACCACTCTCGGTGCAAG 480
Db 421 GCGCTGGTCACTCCCTGGGACAGTGTATCTTTGCTGGGACCACTCTCGGTGCAAG 480
Qy 481 ACGGCGCTCTCTGTGAGAGCTTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540
Db 481 ACGGCGCTCTCTGTGAGAGCTTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540
Qy 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCAATCTTATTTGCTCTCTTCAAGATTGT 600
Db 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCAATCTTATTTGCTCTCTTCAAGATTGT 600
Qy 601 TGGAGCTGAGGCGGAGGACAGCTGCGGACAGGCTCGGATGAGAGGCGACCGG 660
Db 601 TGGAGCTGAGGCGGAGGACAGCTGCGGACAGGCTCGGATGAGAGGCGACCGG 660
Qy 661 TTCAATCGTGGTGGCAATTTGTGTCATCATGCTACCTGCGGCGAGGCTGTCTGTAGA 720
Db 661 TTCAATCGTGGTGGCAATTTGTGTCATCATGCTACCTGCGGCGAGGCTGTCTGTAGA 720
Qy 721 CTCTATTCTCTGAGCGTGGCTCGAGTGGCTGCGATGCTCTGTCCATGGGCGCTG 780
Db 721 CTCTATTCTCTGAGCGTGGCTCGAGTGGCTGCGATGCTCTGTCCATGGGCGCTG 780
Qy 781 CACATAACCTTCAGCTTCACTTACATGAAAGCATGCTGGATCCCTGGTGTATTATTT 840
Db 781 CACATAACCTTCAGCTTCACTTACATGAAAGCATGCTGGATCCCTGGTGTATTATTT 840
Qy 841 TCAAGCCCTCTCTTCCAAATTTACAAAGCTCAAAATCTGAGTCTGAAACCCCAAG 900
Db 841 TCAAGCCCTCTCTTCCAAATTTACAAAGCTCAAAATCTGAGTCTGAAACCCCAAG 900
Qy 901 CAGCAGGACACTCACAAGACAAAGGCGGAGAGATGCAATTTGAACTCGGTGCG 960
Db 901 CAGCAGGACACTCACAAGACAAAGGCGGAGAGATGCAATTTGAACTCGGTGCG 960
Qy 961 AGGAGTTGCATGAGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020
Db 961 AGGAGTTGCATGAGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020
Qy 1021 CACATGTTGAGTGGCAC 1038
Db 1021 CACATGTTGAGTGGCAC 1038
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## RESULT 2

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US-10-076-260-1
; Sequence 1, Application US/10076260
; Publication No. US20030171541A1
; GENERAL INFORMATION:
; APPLICANT: Eliott, Steven G.
; APPLICANT: Rogers, No. US20030171541A1ma
; APPLICANT: Busse, Leigh Anne
; TITLE OF INVENTION: G-Protein Coupled Receptor Molecules and Uses Thereof
; FILE REFERENCE: 02-076
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US/10/076,260
; PRIOR APPLICATION NUMBER: 60/269,040
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; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1038)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTACACGGGTGCTGCTGCGCATCGAGGGGGACACCATCTCCAGCTGATGCCCGCG 60
Db 1 ATGTACACGGGTGCTGCTGCGCATCGAGGGGGACACCATCTCCAGCTGATGCCCGCG 60
Qy 61 CTGCTCATTTGGGCTTTGCTGCTGGGCGCACTAGGCAATGGGCTGCGCTGTGTTTC 120
Db 61 CTGCTCATTTGGGCTTTGCTGCTGGGCGCACTAGGCAATGGGCTGCGCTGTGTTTC 120
Qy 121 TGGTCCACATGACACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCCCTGGCT 180
Db 121 TGGTCCACATGACACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCCCTGGCT 180
Qy 181 GATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTACTCAGAGCTAGACAC 240
Db 181 GATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTACTCAGAGCTAGACAC 240
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Db 241 TGGGCTTTTGGGACATTCCTTGGGAGTGGGCTCTTCACTGGCCCATGAAAGGGCC 300
Qy 301 GGGAGCATGCTGTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAAGTGGTCCACCCC 360
Db 301 GGGAGCATGCTGTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAAGTGGTCCACCCC 360
Qy 361 CACACCGGCTGAAACATCTATCTCCACCGGCTGGGCTGGCATCGTCTGCACCTGTGG 420
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Qy 421 GCGCTGCTCATCTCGGACAGTGTATCTTTGCTGGGAAACCATCTCTGGTGGCAAGAG 480
Db 421 GCGCTGCTCATCTCGGAAACAGTGTATCTTTGCTGGGAAACCATCTCTGGTGGCAAGAG 480
Qy 481 ACGGCGCTCTCTGTGAGAGCTTCATCATGAGTGGGCAATGGCTGGCATGACATCATG 540
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Qy 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCAATCTTATTTGCTCTCTTCAAGATTGT 600
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Qy 601 TGGAGCTGAGGCGGAGGACAGCTGCGGACAGGCTCGGATGAGAGGCGACCGG 660
Db 601 TGGAGCTGAGGCGGAGGACAGCTGCGGACAGGCTCGGATGAGAGGCGACCGG 660
Qy 661 TTCAATCGTGGTGGCAATTTGTTTCATCATGCTACCTGCGGCGAGGCTGTCTGTAGA 720
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Qy 721 CTCTATTCTCTGAGCGTGGCTCGAGTGGCTGCGATGCTCTGTCCATGGGCGCTG 780
Db 721 CTCTATTCTCTGAGCGTGGCTCGAGTGGCTGCGATGCTCTGTCCATGGGCGCTG 780
Qy 781 CACATAACCTTCAGCTTCACTTACATGAAAGCATGCTGGATCCCTGGTGTATTATTT 840
Db 781 CACATAACCTTCAGCTTCACTTACATGAAAGCATGCTGGATCCCTGGTGTATTATTT 840
Qy 841 TCAAGCCCTCTCTTCCAAATTTCTACAAAGCTCAAAATCTGAGTCTGAAACCCCAAG 900
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Db 841 TCAAGCCCTCTCTTCCCAATCTCAACAAGCTCAAAATCTGAGTCTGAAACCCAG 900  
Qy 901 CAGCCAGGACACTCAAAAACAAAAGCCGGAAGAGATGCCAATTCGAACCTCGTCCG 960  
Db 901 CAGCCAGGACACTCAAAAACAAAAGCCGGAAGAGATGCCAATTCGAACCTCGTCCG 960  
Qy 961 AGGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTCATGGGCAATGGATCCC 1020  
Db 961 AGGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTCATGGGCAATGGATCCC 1020  
Qy 1021 CACATTTTTCAGTGGCAC 1038  
Db 1021 CACATTTTTCAGTGGCAC 1038

## RESULT 3

US-10-332-032-2  
; Sequence 2, Application US/10332032  
; Publication No. US20040086940A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptor Protein and its DNA  
; FILE REFERENCE: F2001-154PCT  
; CURRENT APPLICATION NUMBER: US/10/332,032  
; PRIOR FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: JP 2000-206860  
; PRIOR FILING DATE: 2000-07-04  
; PRIOR APPLICATION NUMBER: JP 2000-235274  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 5  
; SEQ ID NO 2  
; LENGTH: 1038  
; TYPE: DNA  
; ORGANISM: Human  
US-10-332-032-2

Query Match 100.0%; Score 1038; DB 17; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTACACGGGTCTGTGCTGCCGCTCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Db 1 ATGTACACGGGTCTGTGCTGCCGCTCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Qy 61 CTGCTCATGTGCGCTTTGTGCTGCGCGCACTAGGCAATGGGTGCGCCCTGTGTTTC 120  
Db 61 CTGCTCATGTGCGCTTTGTGCTGCGCGCACTAGGCAATGGGTGCGCCCTGTGTTTC 120  
Qy 121 TGCCTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCGGTGGCT 180  
Db 121 TGCCTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCGGTGGCT 180  
Qy 181 GATTTCCCTCTATGATCTGCTGCTTTTCGGAAGACTATTAATCTCAGAGTAGACAC 240  
Db 181 GATTTCCCTCTATGATCTGCTGCTTTTCGGAAGACTATTAATCTCAGAGTAGACAC 240  
Qy 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTCACGTGGCCATGAACGGGCC 300  
Db 241 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTCACGTGGCCATGAACGGGCC 300  
Qy 301 GGGAGCATCGTGTCTTACGCTGTGCTGCGGACAGGTATTTCAAAAGTGGTCCACCCC 360  
Db 301 GGGAGCATCGTGTCTTACGCTGTGCTGCGGACAGGTATTTCAAAAGTGGTCCACCCC 360  
Qy 361 CACCAAGGGTGAACATCTCTCAACCGGTGGCGGTGGCATCTGTCACCTGTGG 420  
Db 361 CACCAAGGGTGAACATCTCTCAACCGGTGGCGGTGGCATCTGTCACCTGTGG 420  
Qy 421 GCCCTGGTCACTCTGGGAACAGTGTATCTTTTGTGGAGAACCACTCTGGGTGCAAG 480  
Db 421 GCCCTGGTCACTCTGGGAACAGTGTATCTTTTGTGGAGAACCACTCTGGGTGCAAG 480

Qy 481 ACGGCGCTCTCTCTGAGAGCTTTCATGAGTGGGCAATGAGTGGCATGACATCATG 540  
Db 481 ACGGCGCTCTCTCTGAGAGCTTTCATGAGTGGGCAATGAGTGGCATGACATCATG 540  
Qy 541 TTCAGCTGGAGTCTTTTATGCCCTCGGCATCATCTTATTTGCTCTCTTCAAGATGTT 600  
Db 541 TTCAGCTGGAGTCTTTTATGCCCTCGGCATCATCTTATTTGCTCTCTTCAAGATGTT 600  
Qy 601 TGGAGCTGAGGCGGAGGAGAGCTGCGGACAGAGCTGCGGATGAAGAGGAGGAGCCGG 660  
Db 601 TGGAGCTGAGGCGGAGGAGAGCTGCGGACAGAGCTGCGGATGAAGAGGAGGAGCCGG 660  
Qy 661 TTCATCATGTTGGTGGCAATTTGTTTTCATCATGCTGCTGCGGAGGCTGTCTGCTAGA 720  
Db 661 TTCATCATGTTGGTGGCAATTTGTTTTCATCATGCTGCTGCGGAGGCTGTCTGCTAGA 720  
Qy 721 CTCTATTTCTCTGAGCGGTGCCCTCGAGTGGGCTGCGATCCCTCTGTCATGGGCGCTG 780  
Db 721 CTCTATTTCTCTGAGCGGTGCCCTCGAGTGGGCTGCGATCCCTCTGTCATGGGCGCTG 780  
Qy 781 CACATAACCTCAGCTTTCACCTACATGAACAGCATGCTGGATCCCTGCTGTATTTT 840  
Db 781 CACATAACCTCAGCTTTCACCTACATGAACAGCATGCTGGATCCCTGCTGTATTTT 840  
Qy 841 TCAAGCCCTCTCTTCCAAATTTCTACHAAGCTCAAAATCTGAGTCTGAAACCCAG 900  
Db 841 TCAAGCCCTCTCTTCCAAATTTCTACHAAGCTCAAAATCTGAGTCTGAAACCCAG 900  
Qy 901 CAGCCAGGACACTCAAAAACAAAAGCCGGAAGAGATGCCAATTTGGAACCTCGTCCG 960  
Db 901 CAGCCAGGACACTCAAAAACAAAAGCCGGAAGAGATGCCAATTTGGAACCTCGTCCG 960  
Qy 961 AGGAGTTCATGAGTGTGGCAATAGTTTCCAAAGCCAGTCTCATGGGCAATGGATCCC 1020  
Db 961 AGGAGTTCATGAGTGTGGCAATAGTTTCCAAAGCCAGTCTCATGGGCAATGGATCCC 1020  
Qy 1021 CACATTTTTCAGTGGCAC 1038  
Db 1021 CACATTTTTCAGTGGCAC 1038

## RESULT 4

US-09-862-274-1  
; Sequence 1, Application US/09862274  
; Patent No. US20020052022A1  
; GENERAL INFORMATION:  
; APPLICANT: ELSHOURBAGY, NABIL  
; APPLICANT: GATTU, MAHANANDESHWAR  
; APPLICANT: SHABON, USMAN  
; APPLICANT: IGNAF, DIANE MICHELE  
; TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE  
; TITLE OF INVENTION: 7TMR (AXOR87)  
; FILE REFERENCE: GP-70703-1  
; CURRENT APPLICATION NUMBER: US/09/862,274  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 09/580,675  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: GB 0026839.1  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1041  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-862-274-1

Query Match 100.0%; Score 1038; DB 9; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTACACGGGTCTGTGCTGCCGCTCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Db 1 ATGTACACGGGTCTGTGCTGCCGCTCGAGGGGACACCATCTCCAGGTGATCGCGCG 60

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Db 1 ATGTAAAGGGTCTGTGCTGCGCATCGAGGGGAGACCAATCTCCAGGTGATGCGCGG 60
Qy 61 CTGCTCATTTGGGCTTTGGTGGCGGCACTAGGCAATGGGCTGGCCCTGTGTGTTTC 120
Db 61 CTGCTCATTTGGGCTTTGGTGGCGGCACTAGGCAATGGGCTGGCCCTGTGTGTTTC 120
Qy 121 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180
Db 121 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180
Qy 181 GATTTCTCTTATGATCTGCTGCTCTTTTGGAGACATATTACCTCAGAGCTAGACAC 240
Db 181 GATTTCTCTTATGATCTGCTGCTCTTTTGGAGACATATTACCTCAGAGCTAGACAC 240
Qy 241 TGGGCTTTTGGGCAATTCCTTCCGAGTGGGCTCTTACGTTGGCCATGAACAGGCC 300
Db 241 TGGGCTTTTGGGCAATTCCTTCCGAGTGGGCTCTTACGTTGGCCATGAACAGGCC 300
Qy 301 GGGAGCATCGTGTCTTACCGGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Db 301 GGGAGCATCGTGTCTTACCGGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Qy 361 CACCAAGCGGTGAACATCTCCACCGGCTGGCGGTGGCGCTGGCATGCTGCAACCTTGG 420
Db 361 CACCAAGCGGTGAACATCTCTTCCACCGGCTGGCGGTGGCGCTGGCATGCTGCAACCTTGG 420
Qy 421 GCCCTGCTCATGAGAGCTTGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 480
Db 421 GCCCTGCTCATGAGAGCTTGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 480
Qy 481 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 540
Db 481 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 540
Qy 541 TTCCAGCTGAGTCTTTATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 600
Db 541 TTCCAGCTGAGTCTTTATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 600
Qy 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCCACCCGG 660
Db 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCCACCCGG 660
Qy 661 TTCAATCATGTTGGTGGCAATTTGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TTCAATCATGTTGGTGGCAATTTGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 CTCTATTTCTCTGGAAGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 780
Db 721 CTCTATTTCTCTGGAAGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 780
Qy 781 CACATAACCTCAGCTTCACTATGAAAGAGATGCTGGAATCCCTGCTGCTGCTGCTGCTGCT 840
Db 781 CACATAACCTCAGCTTCACTATGAAAGAGATGCTGGAATCCCTGCTGCTGCTGCTGCTGCT 840
Qy 841 TCAAGCCCTCTTCTCCCAATTTCTACAAAGCTCAAAATCTGAGTCTGAAACCCAG 900
Db 841 TCAAGCCCTCTTCTCCCAATTTCTACAAAGCTCAAAATCTGAGTCTGAAACCCAG 900
Qy 901 CAGCCAGGACACTCAAAAACAAAGGCCGGAAGAGATGCCAATTTGAACTCTCGGTGCG 960
Db 901 CAGCCAGGACACTCAAAAACAAAGGCCGGAAGAGATGCCAATTTGAACTCTCGGTGCG 960
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Qy 1021 CACATTTGTTGAGTGGCAC 1038
Db 1021 CACATTTGTTGAGTGGCAC 1038
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; Sequence 1, Application US/09886041
; Publication No. US20030059869A1
; GENERAL INFORMATION:
; APPLICANT: XIA, TAI-HE
; APPLICANT: NI, DONGHUI
; APPLICANT: EISHINGDELO, HAIFENG
; APPLICANT: ARDATI, ALI
; APPLICANT: MINNICH, ANNE
; APPLICANT: JUPPE, RAY
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 41491
; CURRENT APPLICATION NUMBER: US/09/886,041
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent ver. 2.1
; SEQ ID NO 1
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-886-041-1
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Query Match 100.0%; Score 1038; DB 10; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTACAAAGGGTCTGTGCTGCGCATCGAGGGGAGACCAATCTCCAGGTGATGCGCGG 60
Db 1 ATGTACAAAGGGTCTGTGCTGCGCATCGAGGGGAGACCAATCTCCAGGTGATGCGCGG 60
Qy 61 CTGCTCATTTGGGCTTTGGTGGCGCACTAGGCAATGGGCTGGCCCTGTGTGTTTC 120
Db 61 CTGCTCATTTGGGCTTTGGTGGCGCACTAGGCAATGGGCTGGCCCTGTGTGTTTC 120
Qy 121 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180
Db 121 TGGTTCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCCCTGGCT 180
Qy 181 GATTTCTCTTATGATCTGCTGCTCTTTTGGAGACATATTACCTCAGAGCTAGACAC 240
Db 181 GATTTCTCTTATGATCTGCTGCTCTTTTGGAGACATATTACCTCAGAGCTAGACAC 240
Qy 241 TGGGCTTTTGGGCAATTCCTTCCGAGTGGGCTCTTACGTTGGCCATGAACAGGCC 300
Db 241 TGGGCTTTTGGGCAATTCCTTCCGAGTGGGCTCTTACGTTGGCCATGAACAGGCC 300
Qy 301 GGGAGCATCGTGTCTTACCGGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Db 301 GGGAGCATCGTGTCTTACCGGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Qy 361 CACCAAGCGGTGAACATCTCCACCGGCTGGCGGTGGCGCTGGCATGCTGCAACCTTGG 420
Db 361 CACCAAGCGGTGAACATCTCTTCCACCGGCTGGCGGTGGCGCTGGCATGCTGCAACCTTGG 420
Qy 421 GCCCTGCTCATGAGAGCTTGAAGCCAGGTGATCTTTTGGAGAACCAATCTCTCGTGCAGAG 480
Db 421 GCCCTGCTCATGAGAGCTTGAAGCCAGGTGATCTTTTGGAGAACCAATCTCTCGTGCAGAG 480
Qy 481 ACAGCCGCTCTCTGTGAGAGCTTTCATCATGAGTGGCCCAATGGCTGGCATGATCATG 540
Db 481 ACAGCCGCTCTCTGTGAGAGCTTTCATCATGAGTGGCCCAATGGCTGGCATGATCATG 540
Qy 541 TTCCAGCTGAGTCTTTATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 600
Db 541 TTCCAGCTGAGTCTTTATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 600
Qy 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCCACCCGG 660
Db 601 TGGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCCACCCGG 660
Qy 661 TTCAATCATGTTGGTGGCAATTTGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TTCAATCATGTTGGTGGCAATTTGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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; Sequence 7, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1041)
US-10-343-650A-7

Query Match      100.0%; Score 1038; DB 13; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60
DB 1 ATGTACACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60
QY 61 CTGCTCATGTGGCCCTTTGTGCTGGGCGCAGTAGGCATAGGGTGCCTGTGTGTTT 120
DB 61 CTGCTCATGTGGCCCTTTGTGCTGGGCGCAGTAGGCATAGGGTGCCTGTGTGTTT 120
QY 121 TGCCTCCACATGAAGACCTCGAAGCCAGCAGCTGTTTACCTTTCAATTTGGCGTGCCT 180
DB 121 TGCCTCCACATGAAGACCTCGAAGCCAGCAGCTGTTTACCTTTCAATTTGGCGTGCCT 180
QY 181 GATTTCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GATTTCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 TGGGCTTTTGGGACATTCCTTCGAGTGGGCTCTTTCAGTTGGCCATGAACAGGCCC 300
DB 241 TGGGCTTTTGGGACATTCCTTCGAGTGGGCTCTTTCAGTTGGCCATGAACAGGCCC 300
QY 301 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGGGACAGGATTTTCAAGTGGTCCACCCC 360
DB 301 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGGGACAGGATTTTCAAGTGGTCCACCCC 360
QY 361 CACCACGGGTGAACACTATCTCCACCGGGTGGGCTGGCATCGTCTGACCCCTGTGG 420
DB 361 CACCACGGGTGAACACTATCTCCACCGGGTGGGCTGGCATCGTCTGACCCCTGTGG 420
QY 421 GCGTGTCTATCTCGGAAAGTGTATCTTTGCTGGAGACCATCTCTGGTGCAGAG 480
DB 421 GCGTGTCTATCTCGGAAAGTGTATCTTTGCTGGAGACCATCTCTGGTGCAGAG 480
QY 481 ACGCCCTCTCTGTGAGAGCTTCATCATGAGTTCGCGCAATGGCTGCGATGACATCATG 540
DB 481 ACGCCCTCTCTGTGAGAGCTTCATCATGAGTTCGCGCAATGGCTGCGATGACATCATG 540
QY 541 TTCAGCTGAGTCTTTATGCCCCCTGGCATCATCTTATTTTCTCTCTTCAAGATTGTT 600
DB 541 TTCAGCTGAGTCTTTATGCCCCCTGGCATCATCTTATTTTCTCTCTTCAAGATTGTT 600
QY 601 TGGAGCTGAGGGCGGAGCAGCTGCGGACAGAGCTGGATGAAGAGGACCCGG 660
DB 601 TGGAGCTGAGGGCGGAGCAGCTGCGGACAGAGCTGGATGAAGAGGACCCGG 660
QY 661 TTCCATGCTGTGGCAATTGTTTCATCATGCTTACCTGCGCCAGCGTCTGCTAGA 720
DB 661 TTCCATGCTGTGGCAATTGTTTCATCATGCTTACCTGCGCCAGCGTCTGCTAGA 720

; Sequence 1, Application US/10188149A
; Publication No. US2003007734A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000782-CON
; CURRENT APPLICATION NUMBER: US/10/188,149A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 09/666,535
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/230,459
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/192,419
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-149A-1

Query Match      100.0%; Score 1038; DB 15; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60
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DB 121 TGCCTCCACATGAAGACCTCGAAGCCAGCAGCTGTTTACCTTTCAATTTGGCGTGCCT 180
QY 181 GATTTCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GATTTCTCTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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QY 241 TGGGCTTTTGGGACATTCCTCCGAGTGGGCTCTTCACTGTTGCCCATGAACAGGGCC 300
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QY 301 GGGAGCATCGTCTTCTTAAGTGGTGGCTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Db 301 GGGAGCATCGTCTTCTTAAGTGGTGGCTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
QY 361 CACCAACGGGTGAAACATATCTCCACCCGGGTGGGCTGGCATCGTCTGCAACCGTGG 420
Db 361 CACCAACGGGTGAAACATATCTCCACCCGGGTGGGCTGGCATCGTCTGCAACCGTGG 420
QY 421 GCGCTGGTCACTCTGGGAAACAGTATCTTTTCTGGAGAACCATCTCTGCGTGCAGAG 480
Db 421 GCGCTGGTCACTCTGGGAAACAGTATCTTTTCTGGAGAACCATCTCTGCGTGCAGAG 480
QY 481 ACGGCGCTCTCTGAGAGCTTCTATCATGGAGTGGCCCAATGGCTGGCATGACATCATG 540
Db 481 ACGGCGCTCTCTGAGAGCTTCTATCATGGAGTGGCCCAATGGCTGGCATGACATCATG 540
QY 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTTATTTTCTTCAAGATTGTT 500
Db 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTTATTTTCTTCAAGATTGTT 500
QY 601 TGGAGCTGAGCGGAGCGACAGCTGGCCAGACAGGCTCGGATGAAGAAGCGCACCCGG 660
Db 601 TGGAGCTGAGCGGAGCGACAGCTGGCCAGACAGGCTCGGATGAAGAAGCGCACCCGG 660
QY 661 TTCATCATGGTGGGCAATTTGTGTTTCATCATGCTACCTGCTGCTGCTAGAG 720
Db 661 TTCATCATGGTGGGCAATTTGTGTTTCATCATGCTACCTGCTGCTGCTAGAG 720
QY 721 CTCTATTTCCTCTGACAGCTGCTCGAGTGGCTCGCATCTCTGCTGCTGCTGCTGCTG 780
Db 721 CTCTATTTCCTCTGACAGCTGCTCGAGTGGCTCGCATCTCTGCTGCTGCTGCTGCTG 780
QY 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 840
Db 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 840
QY 841 TCAGCGCTCTCTTCCGAAATTTCTACAAAGCTCAAAATCTGCAAGTCTGAACCCCAAG 900
Db 841 TCAGCGCTCTCTTCCGAAATTTCTACAAAGCTCAAAATCTGCAAGTCTGAACCCCAAG 900
QY 901 CAGCAGGACACTCAAAACACAAAGCGCGAGAGATGCCAATTTGCACTCGGTGCG 960
Db 901 CAGCAGGACACTCAAAACACAAAGCGCGAGAGATGCCAATTTGCACTCGGTGCG 960
QY 961 AGGATTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
Db 961 AGGATTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
QY 1021 CACATTCTCAGTGGCAC 1038
Db 1021 CACATTCTCAGTGGCAC 1038
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RESULT 9
US-10-079-384-17
; Sequence 17, Application US/10079384
; Publication No. US20030108966A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1041
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; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (1)..(1041)
; OTHER INFORMATION:
US-10-079-384-17
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Query Match 100.0%; Score 1038; DB 15; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGTACACGGGTCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCGCGCG 60
Db 1 ATGTACACGGGTCTGCTGCTGCGCATCGAGGGGACACCATCTCTCCAGGTGATGCGCGCG 60
QY 61 CTGCTCATTTGTGGCCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCCCTCTGCTGGTTTC 120
Db 61 CTGCTCATTTGTGGCCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCCCTCTGCTGGTTTC 120
QY 121 TCGTTCACATGAAGACCTGGAAGCCACACTGTTTACCTTTCAATTGGCCGTGGCT 180
Db 121 TCGTTCACATGAAGACCTGGAAGCCACACTGTTTACCTTTCAATTGGCCGTGGCT 180
QY 181 GATTTTCCTCTTATCATCTGCGCTGCTTTTCGACAGACTATTTACCTGAGCTAGACAC 240
Db 181 GATTTTCCTCTTATCATCTGCGCTGCTTTTCGACAGACTATTTACCTGAGCTAGACAC 240
QY 241 TGGGCTTTTGGGCAATTTCCCTGCGGAGTGGGGCTCTTCACTGTTGGCCATGAACAGGGCC 300
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QY 301 GGGAGCATGCTGTTCTTTACCGTGGTGGCTGGGCGGTGGCATGCTGCTGCAACCTGCG 360
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QY 361 CACACGCGGTGACACATCTTCCACCGCGGTGGGCGGTGGCATGCTGCTGCAACCTGCG 420
Db 361 CACACGCGGTGACACATCTTCCACCGCGGTGGGCGGTGGCATGCTGCTGCAACCTGCG 420
QY 421 GCCCTGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACCATCTCTGCTGCTGCAAGAG 480
Db 421 GCCCTGGTCACTCTGGGAAACAGTGTATCTTTTGTGGAGAACCATCTCTGCTGCTGCAAGAG 480
QY 481 ACGGCGCTCTCTGAGAGCTTCAATGAGTGGCCCAATGGCTGGCATGACATCATG 540
Db 481 ACGGCGCTCTCTGAGAGCTTCAATGAGTGGCCCAATGGCTGGCATGACATCATG 540
QY 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTATTTTCTGCTTCAAGATTGTT 600
Db 541 TTCCAGCTGGAGTCTTTATGCGCTCGGCATCATCTTATTTTCTGCTTCAAGATTGTT 600
QY 601 TGGAGCTGAGCGGAGCGACAGCTGCGCCAGACAGGCTCGGATGAAGAAGCGCACCCGG 660
Db 601 TGGAGCTGAGCGGAGCGACAGCTGCGCCAGACAGGCTCGGATGAAGAAGCGCACCCGG 660
QY 661 TTCAATCATGGTGGGCAATTTGTGTTTCATCATGCTACCTGCTGCTGCTAGAG 720
Db 661 TTCAATCATGGTGGGCAATTTGTGTTTCATCATGCTACCTGCTGCTGCTAGAG 720
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QY 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 840
Db 781 CACATAACCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 840
QY 841 TCAAGCGCTCTCTTCCGAAATTTCTACAAAGCTCAAAATCTGCAAGTCTGAACCCCAAG 900
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Db 961 AGGAGTTGATCAGTGTGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATCCC 1020
QY 1021 CACATTGTTGAGTGGCAC 1038
Db 1021 CACATTGTTGAGTGGCAC 1038

RESULT 10
US-10-321-807-23
; Sequence 23, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-23

Query Match 100.0%; Score 1038; DB 15; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGAGTGATGCCGCG 60
Db 1 ATGTACAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGAGTGATGCCGCG 60
QY 61 CTGCTCATTTGGCTTTGCTGGGCGCATAGGCAATGGGTGCGCCCTGTGTGTTTC 120
Db 61 CTGCTCATTTGGCTTTGCTGGGCGCATAGGCAATGGGTGCGCCCTGTGTGTTTC 120
QY 121 TGCTTCACATGAAGACCTGGAGCCCGACGACTGTTTACCTTTTCATTTGGCGTGCGCT 180
Db 121 TGCTTCACATGAAGACCTGGAGCCCGACGACTGTTTACCTTTTCATTTGGCGTGCGCT 180
QY 181 GATTTCCTCTTATGATCTGCTTGGCTTTTCGGACAGACTTACCTTCAGACCTAGACAC 240
Db 181 GATTTCCTCTTATGATCTGCTTGGCTTTTCGGACAGACTTACCTTCAGACCTAGACAC 240
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QY 241 TGGGCTTTTGGGACATTTCCCTGCCAGTGGGGCTCTTTCACGTTGGCCATCAACAGGGCC 300
Db 241 TGGGCTTTTGGGACATTTCCCTGCCAGTGGGGCTCTTTCACGTTGGCCATCAACAGGGCC 300
QY 301 GGGAGCATCGTGTTCCTTACGTTGGGTGGCTGGCGACAGGTATTTCAAGTGGTCCACCC 360
Db 301 GGGAGCATCGTGTTCCTTACGTTGGGTGGCTGGCGACAGGTATTTCAAGTGGTCCACCC 360
QY 361 CACCAACGGGTGAACACTATCTCCACCCGGGTGGCGGTGGCATCGTCTGCACCTGTGG 420
Db 361 CACCAACGGGTGAACACTATCTCCACCCGGGTGGCGGTGGCATCGTCTGCACCTGTGG 420
QY 421 GCGCTGGTCACTCTGGGAAACAGTGTATCTTTTGTCTGGAGAACCATCTCTGCGTGCAGAG 480
Db 421 GCGCTGGTCACTCTGGGAAACAGTGTATCTTTTGTCTGGAGAACCATCTCTGCGTGCAGAG 480
QY 481 AGCGCGCTCTCTCTGAGAGCTTTCATCATGGAGTGGCCCAATGGCTGGCATGACATCATG 540
Db 481 AGCGCGCTCTCTCTGAGAGCTTTCATCATGGAGTGGCCCAATGGCTGGCATGACATCATG 540
QY 541 TTCCAGCTGGAGTTCCTTATGCCCCCTCGGCATCATCTTATTTTGTCTCTTCAAGATTGT 600
Db 541 TTCCAGCTGGAGTTCCTTATGCCCCCTCGGCATCATCTTATTTTGTCTCTTCAAGATTGT 600
QY 601 TGGAGCCTGAGCGGAGGAGGAGGAGCTGGCCAGACAGGCTGGATGAAGAGGAGCCCGG 660
Db 601 TGGAGCCTGAGCGGAGGAGGAGGAGCTGGCCAGACAGGCTGGATGAAGAGGAGCCCGG 660
QY 661 TTCCATCATGGTGGTGGCAATTTGTGTTTCATCATGCTACCTGCCAGCTGTCTGTAGA 720
Db 661 TTCCATCATGGTGGTGGCAATTTGTGTTTCATCATGCTACCTGCCAGCTGTCTGTAGA 720
QY 721 CTCTATTTCTCTGAGACGGTGGCTTCGAGTGGCTCGGATCCCTCTGTCCATGGGGCCCTG 780
Db 721 CTCTATTTCTCTGAGACGGTGGCTTCGAGTGGCTCGGATCCCTCTGTCCATGGGGCCCTG 780
QY 781 CACATAACCTCTCAGCTTCACTTACATGAACAGCAGCTGGATGCCCTCTGTCCATGGGGCCCTG 840
Db 781 CACATAACCTCTCAGCTTCACTTACATGAACAGCAGCTGGATGCCCTCTGTCCATGGGGCCCTG 840
QY 841 TCAAGCCCTCTCTTTCCAAATTTTACAAAGCTCAAAATCTGCAAGTCTGAAACCCAG 900
Db 841 TCAAGCCCTCTCTTTCCAAATTTTACAAAGCTCAAAATCTGCAAGTCTGAAACCCAG 900
QY 901 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGTGGCAATTTCCAACTCGGTGCG 960
Db 901 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGTGGCAATTTCCAACTCGGTGCG 960
QY 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATCCC 1020
Db 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATCCC 1020
QY 1021 CACATTGTTGAGTGGCAC 1038
Db 1021 CACATTGTTGAGTGGCAC 1038
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RESULT 11
US-10-210-172-177
; Sequence 177, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
```

APPLICANT: Casman, Stacie  
APPLICANT: Voss, Edward  
APPLICANT: Boldog, Ferenc  
APPLICANT: Gorman, Linda  
APPLICANT: Leite, Mario  
APPLICANT: Vernet, Corine  
APPLICANT: Anderson, David  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zhong, Wei  
APPLICANT: Gerlach, Valerie  
APPLICANT: Hjalte, Tord  
APPLICANT: Pastelli, Luca  
APPLICANT: Spytek, Kimberly  
APPLICANT: Edinger, Shlomit  
APPLICANT: Ellerman, Karen  
APPLICANT: Malyankar, Uriel  
APPLICANT: MacDougall, John  
APPLICANT: Stone, David  
APPLICANT: Alsobrook II, John  
APPLICANT: Lepley, Denise et al.  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-416 A  
CURRENT APPLICATION NUMBER: US/10/210,172  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/309,501  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/323,994  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/373,814  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 60/310,291  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 60/310,951  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/310,544  
PRIOR FILING DATE: 2001-08-07  
PRIOR APPLICATION NUMBER: 60/311,292  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/311,979  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/313,201  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 60/312,892  
PRIOR FILING DATE: 2001-08-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 327  
SOFTWARE: CuraSeqList version 0.1  
SEQ ID NO 177  
LENGTH: 1050  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (6)..(1043)  
US-10-210-172-177

Query Match 100.0%; Score 1038; DB 13; Length 1050;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTGTGTGGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60  
Db 6 ATGTACACGGGTGTGTGGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 65  
QY 61 CTGCTCATTTGGCTTTGTCTGGCGCATAGGCATGGGTGGCCCTGTGTGGTTTC 120  
Db 66 CTGCTCATTTGGCTTTGTCTGGCGCATAGGCATGGGTGGCCCTGTGTGGTTTC 125  
QY 121 TGTTCACATGAAGACCTGGAAGCCGACGCTGTCTTACCTTTTCAATTTGGCCGTGGCT 180  
Db 126 TGTTCACATGAAGACCTGGAAGCCGACGCTGTCTTACCTTTTCAATTTGGCCGTGGCT 185  
QY 181 GATTTCTCTTATGATCTGCCTGCCTTTTCGGGACAGACTATTACCTCAGACGTAGACAC 240

Db 186 GATTTCTCTTATGATCTGCCTGCCTTTTCGGGACAGACTATTACCTCAGACGTAGACAC 245  
QY 241 TGGGCTTTTGGGACATTCCTTGCAGAGTGGGGCTCTTCACTTGGCCATGAACAGGGCC 300  
Db 246 TGGGCTTTTGGGACATTCCTTGCAGAGTGGGGCTCTTCACTTGGCCATGAACAGGGCC 305  
QY 301 GGGAGCATCGTGTTCCTTACGGTGGTGGCGGACAGGATTTTCAAAGTGGTCCACCCC 360  
Db 306 GGGAGCATCGTGTTCCTTACGGTGGTGGCGGACAGGATTTTCAAAGTGGTCCACCCC 365  
QY 361 CACCACGCGGTGAACACTATCTCCACCCGGTGGCGGCTGGCATCGTTCGACCTGTGG 420  
Db 366 CACCACGCGGTGAACACTATCTCCACCCGGTGGCGGCTGGCATCGTTCGACCTGTGG 425  
QY 421 GCCTGTCTATCTCTGGGACAGGTGTATCTTTTGTGGAGAACCATCTCTGGTGCACAGAG 480  
Db 426 GCCTGTCTATCTCTGGGACAGGTGTATCTTTTGTGGAGAACCATCTCTGGTGCACAGAG 485  
QY 481 ACGGCGCTCTCTGTGAGAGCTTCATCATGGAGTTCGGCCAAATGGCTGGCATGACATG 540  
Db 486 ACGGCGCTCTCTGTGAGAGCTTCATCATGGAGTTCGGCCAAATGGCTGGCATGACATG 545  
QY 541 TTCAGCTGGAGTTCCTTTATGCCCCCTGGCCATCATCTTATTTTGGCTCTTCAAGATTT 600  
Db 546 TTCAGCTGGAGTTCCTTTATGCCCCCTGGCCATCATCTTATTTTGGCTCTTCAAGATTT 605  
QY 601 TGGAGCTTGAAGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCGGCCGG 660  
Db 606 TGGAGCTTGAAGCGGAGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAGGCGGCCGG 665  
QY 661 TTCATCATGGTGGCAATTTGTTTCATCATGCTTACCTGCCAGCGTGTCTGTCTAGA 720  
Db 666 TTCATCATGGTGGCAATTTGTTTCATCATGCTTACCTGCCAGCGTGTCTGTCTAGA 725  
QY 721 CTCATTTCTCTGAGCGGTGCGCTCGAGTGCCTCGATCCCTCTCTGCCATGGGCGCTG 780  
Db 726 CTCATTTCTCTGAGCGGTGCGCTCGAGTGCCTCGATCCCTCTCTGCCATGGGCGCTG 785  
QY 781 CACATAACCTCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 840  
Db 786 CACATAACCTCTCAGCTTCACTACATGAACAGCATGCTGGATCCCTGGTGTATTTT 845  
QY 841 TCAGGCGCTCTCTTCCGAAATTTTACAAACAGCTCAAAATCTGCAAGTCTGAAACCCAG 900  
Db 846 TCAGGCGCTCTCTTCCGAAATTTTACAAACAGCTCAAAATCTGCAAGTCTGAAACCCAG 905  
QY 901 CAGCCAGGACACTCAAAAACACAAAGGCGGAGAGATGCCAATTTGCACTCGGTGCGC 960  
Db 906 CAGCCAGGACACTCAAAAACACAAAGGCGGAGAGATGCCAATTTGCACTCGGTGCGC 965  
QY 961 AGGAGTTGATCAGTGTGGCAAAATAGTTTCCAAAGCAGTCTGATGGGCAATGGGATCCC 1020  
Db 966 AGGAGTTGATCAGTGTGGCAAAATAGTTTCCAAAGCAGTCTGATGGGCAATGGGATCCC 1025  
QY 1021 CACATTTGTGAGTGGCAC 1038  
Db 1026 CACATTTGTGAGTGGCAC 1043

RESULT 12  
US-10-044-643-1  
; Sequence 1, Application US/10044643  
; Publication No. US2003019535A1  
; GENERAL INFORMATION:  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Vernet, Corine  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Wolenc, Adam R  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishnu, Vishnu S  
; APPLICANT: Tchernev, Velizar T

	Query Match	100.0%	Score 1038;	DB 15;	Length 1050;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1038;	Conservative	0;	Mismatches	0;
				Indels	Gaps
QY	1	ATGTACAAACGGGTCTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCCCG	60		
DB	6	ATGTACAAACGGGTCTGCTGCGCATCTGAGGGGACACCATCTCCAGGTGATCGCCCG	65		
QY	61	CTGCTCATTTGTGGCTTTGTCTGGGGCGCACTAGGCCAATGGGGTCGCGCCTGTGTGGTTTC	120		
DB	66	CTGCTCATTTGTGGCTTTGTCTGGGGCGCACTAGGCCAATGGGGTCGCGCCTGTGTGTGGTTTC	125		
QY	121	TGCTTCCACATGAAGACCTGGAAGCCCGACAGACTGTTTACCTTTTTCAAATTTGGCCGTGGCT	180		
DB	126	TGCTTCCACATGAAGACCTGGAAGCCCGACACTGTTTACCTTTTTCAAATTTGGCCGTGGCT	185		
QY	181	GAITTCCTCCTTATGATCTGCTGCCTTTTTCGGACAGACTATATACCTCAGACGTAGACAC	240		
DB	186	GAITTCCTCCTTATGATCTGCTGCCTTTTTCGGACAGACTATATACCTCAGACGTAGACAC	245		
QY	241	TGCGCTTTTGGGGACATTCCTCTGCGAGTGGGGCTCTTTCAGTGTGGGCACTGAACAGAGGCC	300		

RESULT 13

;; TITLE OF INVENTION: No. US20030195335A1el Proteins and Nucleic Acids Encoding Same

;; FILE REFERENCE: 15966-748  
;; CURRENT APPLICATION NUMBER: US/10/044, 643  
;; CURRENT FILING DATE: 2002-01-11  
;; PRIOR APPLICATION NUMBER: 60/193,664  
;; PRIOR FILING DATE: 2000-03-31  
;; PRIOR APPLICATION NUMBER: 60/194,614  
;; PRIOR FILING DATE: 2000-04-05  
;; PRIOR APPLICATION NUMBER: 60/195,063  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,066  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,067  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,068  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,069  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,070  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/195,510  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: 60/219,855  
;; PRIOR FILING DATE: 2000-07-21  
;; PRIOR APPLICATION NUMBER: 60/221,284  
;; PRIOR FILING DATE: 2000-07-27  
;; PRIOR APPLICATION NUMBER: 60/221,325  
;; PRIOR FILING DATE: 2000-07-28  
;; PRIOR APPLICATION NUMBER: 60/224,588  
;; PRIOR FILING DATE: 2000-08-11  
;; PRIOR APPLICATION NUMBER: 60/239,613  
;; PRIOR FILING DATE: 2000-10-11  
;; PRIOR APPLICATION NUMBER: 60/262,508  
;; PRIOR FILING DATE: 2001-01-18  
;; PRIOR APPLICATION NUMBER: 60/263,604  
;; PRIOR FILING DATE: 2001-01-23  
;; PRIOR APPLICATION NUMBER: 60/263,433  
;; PRIOR FILING DATE: 2001-01-23  
;; PRIOR APPLICATION NUMBER: 60/265,161  
;; PRIOR FILING DATE: 2001-01-30  
;; NUMBER OF SEQ ID NOS: 83  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 3  
;; LENGTH: 1050  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-044-643-3

Query Match 100.0%; Score 1038; DB 15; Length 1050;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTGCTGTCGGCATCGAGGGGGACCATCTCCAGGTGATCGCGCG 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
6 ATGTACACGGGTGCTGTCGGCATCGAGGGGGACCATCTCCAGGTGATCGCGCG 65  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 CTGCTCAATGTGGCTTTGTGCTGGCGCAGCTAGGCAATGGGTCGCCCTGTGTGGTTTC 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
66 CTGCTCAATGTGGCTTTGTGCTGGCGCAGCTAGGCAATGGGTCGCCCTGTGTGGTTTC 125  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 TGTTCACATGAGACCTGGAAGCCGACACTGTTTACCTTTTCAATTTGGCCGTGGCT 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
126 TGTTCACATGAGACCTGGAAGCCGACACTGTTTACCTTTTCAATTTGGCCGTGGCT 185  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 GATTCCTCCTTATGATCTGCTGCTTTTCGGACAGACTATTACTCAGACGTAGACAC 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
186 GATTCCTCCTTATGATCTGCTGCTTTTCGGACAGACTATTACTCAGACGTAGACAC 245  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGGCTCTTTCAGTTGGCCATGAAGGGCC 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
246 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGGCTCTTTCAGTTGGCCATGAAGGGCC 305  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 GGGAGCATCGGTTCCTTACCGGTGGTGGCTCGGGACAGGTATTTCAAAGTGGTCCACCC 360

306 GGAGCATCGTGTCTTACGGTGGTGGCTCGGGACAGGTATTTCAAAGTGGTCCACCC 365  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 CACACGGGTGAACACTATCTCCACCCGGGTGGGGCTGGCATCTGCTGCACCTGTGG 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
366 CACACGGGTGAACACTATCTCCACCCGGGTGGGGCTGGCATCTGCTGCACCTGTGG 425  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 GGCCTGCTCATCTCGGGAACAGTATCTTTTCTGGAGAACCATCTCTCGGTGCAAGAG 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
426 GGCCTGCTCATCTCGGGAACAGTATCTTTTCTGGAGAACCATCTCTCTGCTGCAAGAG 485  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
481 ACGGCGCTCTCTGTGTGAGAGCTTTCATCATGAGTTCGGCCCAATGGCTGCTCATCATG 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
486 ACGGCGCTCTCTGTGTGAGAGCTTTCATCATGAGTTCGGCCCAATGGCTGCTCATCATG 545  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
541 TTCAGCTGGAGTTCCTTATGCCCCCTCGGGCATCATCTATTTTGTCTCTTCAAGATTGTT 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
546 TTCAGCTGGAGTTCCTTATGCCCCCTCGGGCATCATCTATTTTGTCTCTTCAAGATTGTT 605  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
601 TGGAGCCTGAGCGGAGGAGGAGCTGGCCAGACAGCTCGGATGAGAGGAGGACCCGG 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
606 TGGAGCCTGAGCGGAGGAGGAGCTGGCCAGACAGCTCGGATGAGAGGAGGACCCGG 665  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
661 TTCATCATGCTGGTGGCAATTTGTGTTTCATCATGCTTACCTGCCAGCGTGTCTGTAGA 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
666 TTCATCATGCTGGTGGCAATTTGTGTTTCATCATGCTTACCTGCCAGCGTGTCTGTAGA 725  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
721 CTCTATTTCTCTGGACGGTGCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
726 CTCTATTTCTCTGGACGGTGCCTCGAGTGCCTCGATCCCTCTGTCCATGGGGCCCTG 785  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
781 CACATAACCTCAGCTTTCACCTACATGAGACAGCATCTGCATCCCTGGGTGATATTTT 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
786 CACATAACCTCAGCTTTCACCTACATGAGACAGCATCTGCATCCCTGGGTGATATTTT 845  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
841 TCAAGCCCTCTCTTTCCCAAATTTCTACAAAGCTCAAAATCTGCACTGTAACCCCAAG 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
846 TCAAGCCCTCTCTTTCCCAAATTTCTACAAAGCTCAAAATCTGCACTGTAACCCCAAG 905  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
901 CAGCCAGGACATCAAAAACACAAAGGCGGAGAGATGCCAATTTGAACTCTGGTGGC 960  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
906 CAGCCAGGACATCAAAAACACAAAGGCGGAGAGATGCCAATTTGAACTCTGGTGGC 965  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
961 AGGAGTTGCATCAGTGTGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGGATCCC 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
966 AGGAGTTGCATCAGTGTGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGGATCCC 1025  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1021 CACATTGTTGAGTGGCAC 1038  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1026 CACATTGTTGAGTGGCAC 1043

RESULT 14  
US-10-210-172-183  
; Sequence 183, Application US/10210172  
; Publication No. US20040043928A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Pena, Carol  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Li, Li  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gorman, Linda  
; APPLICANT: Leite, Mario  
; APPLICANT: Vernet, Corine

```
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Decise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CnraSequid version 0.1
; SEQ ID NO 183
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(1048)
US-10-210-172-183

Query Match 100.0%; Score 1038; DB 13; Length 1057;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTACAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60
Db 11 ATGTACAAACGGGTGCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCG 70
Qy 61 CTGCTCATTTGGCCCTTTGCTGGGCGCACTAGGCAATGGGTCGCCCTGTGGTTTC 120
Db 71 CTGCTCATTTGGCCCTTTGCTGGGCGCACTAGGCAATGGGTCGCCCTGTGGTTTC 130
Qy 121 TGCTTCCACATGAAGACCTGGAAGCCAGACCTGTTTACCTTTTCAATTTGGCCGTGGCT 180
Db 131 TGCTTCCACATGAAGACCTGGAAGCCAGACCTGTTTACCTTTTCAATTTGGCCGTGGCT 190
Qy 181 GATTTCCTCTTATGATCTGCCTGCTTTTGGACAGACTATTACCTCAGACGTAGACAC 240
Db 191 GATTTCCTCTTATGATCTGCCTGCTTTTGGACAGACTATTACCTCAGACGTAGACAC 250
Qy 241 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGCTCTTCAGTTGGCCATGAACAGGGCC 300
Db 251 TGGGCTTTTGGGACATCTCCCTGCGAGTGGGCTCTTCAGTTGGCCATGAACAGGGCC 310
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Qy 301 GGGAGCATCGTGTCTTCTTACCGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 360
Db 311 GGGAGCATCGTGTGTCTTCTTACCGTGGTGGTGGGACAGGTATTTCAAAGTGGTCCACCCC 370
Qy 361 CACCAACGGGTGAACACATCTATCTCCACCGGTGGCGGTGGCATCGTCTGCACCCCTGTGG 420
Db 371 CACCAACGGGTGAACACATCTATCTCCACCGGTGGCGGTGGCATCGTCTGCACCCCTGTGG 430
Qy 421 GCGCTGTCATCTCTGGGAAACAGTGTATCTTTTGTGGAGAACCATCTCTCGGTGCAAGAG 480
Db 431 GCGCTGTCATCTCTGGGAAACAGTGTATCTTTTGTGGAGAACCATCTCTCGGTGCAAGAG 490
Qy 481 ACSCCGTCTCTCTGTAGAGCTTCATCATGAGTGGCCCAATGGCTGCATGACATCATG 540
Db 491 ACSCCGTCTCTCTGTAGAGCTTCATCATGAGTGGCCCAATGGCTGCATGACATCATG 550
Qy 541 TTCCAGCTGGAGTCTCTTTATGCCCTCGGCATCATCTTATTTTGTCTCTCAAGATTGTT 600
Db 551 TTCCAGCTGGAGTCTCTTTATGCCCTCGGCATCATCTTATTTTGTCTCTCAAGATTGTT 610
Qy 601 TGGAGCCTGAGGCGGAGGAGCAGCTGSCCAGACAGAGCTCGGATGAAGAGGCGGCGGG 660
Db 611 TGGAGCCTGAGGCGGAGGAGCAGCTGSCCAGACAGAGCTCGGATGAAGAGGCGGCGGG 670
Qy 661 TTCAATCATGTGTGGCAATTGTGTTTCAATCATGTGTGTTTCAATCATGTGTGTTTCA 720
Db 671 TTCAATCATGTGTGGCAATTGTGTTTCAATCATGTGTGTTTCAATCATGTGTGTTTCA 730
Qy 721 CTCTATTTCTCTGGAACGGTSCCTCGAGTGGCTCGCATCCCTCTGTCTCATGGGCGCTG 780
Db 731 CTCTATTTCTCTGGAACGGTSCCTCGAGTGGCTCGCATCCCTCTGTCTCATGGGCGCTG 790
Qy 781 CAGATTAACCTCAGCTTCACCTACATGAAGAGCATGTGATGCCCTGCTGTTATTTATTT 840
Db 791 CAGATTAACCTCAGCTTCACCTACATGAAGAGCATGTGATGCCCTGCTGTTATTTATTT 850
Qy 841 TCAAGCCCTCTCTTCCCAATTCTCAACAGCTCAAAATCTGCAGTCTCAAAACCCCAAG 900
Db 851 TCAAGCCCTCTCTTCCCAATTCTCAACAGCTCAAAATCTGCAGTCTCAAAACCCCAAG 910
Qy 901 CAGCCAGGACACTCAAAAACACAAAGGCGGAGAGATGCCAATTTGGAACCTCGGTGCG 960
Db 911 CAGCCAGGACACTCAAAAACACAAAGGCGGAGAGATGCCAATTTGGAACCTCGGTGCG 970
Qy 961 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
Db 971 AGGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1030
Qy 1021 CACATTGTTGAGTGGCAC 1038
Db 1031 CACATTGTTGAGTGGCAC 1048

RESULT 15
US-10-210-172-191
; Sequence 191, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
```



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APPLICANT: Leite, Mario
APPLICANT: Vernet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Mei
APPLICANT: Gerlach, Valerie
APPLICANT: Hjal, Tord
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsbrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210,172
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 191
LENGTH: 1057
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1057)
US-10-210-172-191
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Query Match 100.0%; Score 1038; DB 13; Length 1057;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACACGGGTCTGCTCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60
DB 11 ATGTACACGGGTCTGCTCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 70

QY 61 CTGCTCATTTGGCTTTGTCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 120
DB 71 CTGCTCATTTGGCTTTGTCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 130

QY 121 TGCTTCACATGAGACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCGGTGGCT 180
DB 131 TGCTTCACATGAGACCTGGAAGCCAGCACTGTTTACCTTTCAATTTGGCGGTGGCT 190

QY 181 GATTTCCTCTTATGATCTGCTCTCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
DB 191 GATTTCCTCTTATGATCTGCTCTCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 250

QY 241 TGGGCTTTTGGGGACATTTCCCTGCGGAGTGGGGCTCTTTCACTTGGGCCATGACAGGGCC 300
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DB 251 TGGGCTTTTGGGGACATTTCCCTGCGGAGTGGGGCTCTTCACTTGGCCATGACAGGGCC 310
QY 301 GGGAGCATCGTGTTCCTTACGGTGTGGCTGGGACAGGTATTTCAAAGTGTTCACCC 360
DB 311 GGGAGCATCGTGTTCCTTACGGTGTGGCTGGGACAGGTATTTCAAAGTGTTCACCC 370
QY 361 CACACGGGGTGAACACTATCTCCACCCGGGTGGGGCTGGGATCGTCTGCACCTGTGG 420
DB 371 CACACGGGGTGAACACTATCTCCACCCGGGTGGGGCTGGGATCGTCTGCACCTGTGG 430
QY 421 GCCCTGGTCACTCTCGGAAACAGTGTATCTTTTGGCTGGGAAACCATCTCTCGCGTCAAGAG 480
DB 431 GCCCTGGTCACTCTCGGAAACAGTGTATCTTTTGGCTGGGAAACCATCTCTCGCGTCAAGAG 490
QY 481 AGGGCCGTCTCTGTGAGAGCTTCAATCATGAGTGGGCAATGGCTGGGATGACATCATG 540
DB 491 AGGGCCGTCTCTGTGAGAGCTTCAATCATGAGTGGGCAATGGCTGGGATGACATCATG 550
QY 541 TTCCAGCTGGAGTCTCTTTATGCCCTCGGCATCATCTTTATTTTGTCTTCAAGATTGTT 600
DB 551 TTCCAGCTGGAGTCTCTTTATGCCCTCGGCATCATCTTTATTTTGTCTTCAAGATTGTT 610
QY 601 TGGAGCTTGAGCGGAGGAGCAGCTGGCCAGCAGGCTCGGATGAGGAGGCGACCCGG 660
DB 611 TGGAGCTTGAGCGGAGGAGCAGCTGGCCAGCAGGCTCGGATGAGGAGGCGACCCGG 670
QY 661 TTCCATCATGGTGGTGGCAATGTGTTCATCATCATGCTACCTGCCAGCGTGTCTGTCTAG 720
DB 671 TTCCATCATGGTGGTGGCAATGTGTTCATCATCATGCTACCTGCCAGCGTGTCTGTCTAG 730
QY 721 CTCTATTTCTCTGACGCTGCCCTCGAGTGGCTCGGATCCCTCTGTCTCATGGGGCCCTG 780
DB 731 CTCTATTTCTCTGACGCTGCCCTCGAGTGGCTCGGATCCCTCTGTCTCATGGGGCCCTG 790
QY 781 CACATAACCCCTCAGCTTCACTTACATGAAACAGCATGCTGGATCCCTCTGTCTATTTT 840
DB 791 CACATAACCCCTCAGCTTCACTTACATGAAACAGCATGCTGGATCCCTCTGTCTATTTT 850
QY 841 TCAAGCCCTCTCTTTCCCAAAATCTTACAAACAGCTCAAAATCTGCACTGTAACCCCAAG 900
DB 851 TCAAGCCCTCTCTTTCCCAAAATCTTACAAACAGCTCAAAATCTGCACTGTAACCCCAAG 910
QY 901 CAGCCAGGACACTCAAAACACAAAGCGGAGAGATGCCAAATTTTCAAACTCTCGTCCG 960
DB 911 CAGCCAGGACACTCAAAACACAAAGCGGAGAGATGCCAAATTTTCAAACTCTCGTCCG 970
QY 961 AGGAGTTGCACTCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGGATCCC 1020
DB 971 AGGAGTTGCACTCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGTATGGGCAATGGGATCCC 1030
QY 1021 CACATTGTGAGTGGCAC 1038
DB 1031 CACATTGTGAGTGGCAC 1048
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Search completed: July 3, 2004, 10:07:49  
Job time : 565 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 17:15:22 ; Search time 17 Seconds  
(without alignments)  
1059.761 Million cell updates/sec

Title: US-10-076-260-2

Perfect score: 1853

Sequence: 1 MYNGSCCRIGDTISQWPF.....ANSFQSQSDGQWDPHVEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	1	GP81_HUMAN
2	1483	80.0	343	1	GP81_MOUSE
3	880.5	47.5	387	1	HM74_HUMAN
4	448.5	24.2	319	1	GP31_HUMAN
5	371.5	20.0	309	1	CLT2_MOUSE
6	366.5	19.8	346	1	CLT2_HUMAN
7	364	19.6	362	1	P2YR_CHICK
8	364	19.6	362	1	P2YR_MELGA
9	362.5	19.6	373	1	P2YR_BOVIN
10	362	19.5	345	1	CLT2_PIG
11	358.5	19.3	373	1	P2YR_RAT
12	356.5	19.2	373	1	P2YR_CAVPO
13	355.5	19.2	309	1	CLT2_RAT
14	354	19.1	373	1	P2YR_HUMAN
15	351.5	19.0	373	1	P2YR_MOUSE
16	346.5	18.7	370	1	P2Y9_HUMAN
17	340	18.3	344	1	P2Y5_MOUSE
18	339	18.3	308	1	P2Y5_CHICK
19	336	18.1	367	1	GP17_HUMAN
20	327	17.6	309	1	GP35_MOUSE
21	325	17.5	344	1	P2Y5_HUMAN
22	320	17.3	373	1	P2Y2_MOUSE
23	316.5	17.1	374	1	P2Y2_RAT
24	310.5	16.8	420	1	PAR1_XENLA
25	309.5	16.7	363	1	SSR5_RAT
26	308.5	16.6	307	1	GP35_MOUSE
27	308	16.6	340	1	CLT1_PIG
28	307	16.6	391	1	SSR1_MOUSE
29	305.5	16.5	391	1	SSR1_HUMAN
30	305.5	16.5	391	1	SSR1_RAT
31	305	16.5	337	1	CLT1_HUMAN
32	305	16.5	372	1	GP92_HUMAN
33	305	16.5	377	1	P2Y2_HUMAN

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34 304.5 16.4 359 1 AG2R_BOVIN
35 302.5 16.3 369 1 SSR2_HUMAN
36 302 16.3 391 1 BRB2_HUMAN
37 302 16.3 399 1 PAR2_MOUSE
38 300.5 16.2 369 1 SSR2_MOUSE
39 300.5 16.2 369 1 SSR2_RAT
40 300 16.2 328 1 P2Y6_RAT
41 300 16.2 384 1 SSR4_RAT
42 300 16.2 428 1 SSR3_MOUSE
43 299.5 16.2 369 1 SSR2_PIG
44 299 16.1 388 1 SSR4_HUMAN
45 299 16.1 397 1 PAR2_RAT

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#### ALIGNMENTS

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RESULT 1
GP81_HUMAN
ID GP81_HUMAN STANDARD; PRT; 346 AA.
AC Q9BXCO;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable G protein-coupled receptor GPR81.
GN GPR81 OR PKSG80.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
EX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhiko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes."
RL Gene 275:83-91(2001).
[2]
RP SEQUENCE FROM N.A.
EX MEDLINE=22040266; PubMed=12044878;
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence."
RL FEBS Lett. 520:97-101(2002).
[3]
RP SEQUENCE FROM N.A.
RA Wang Y.-G., Gong L.;
RT "Molecular cloning of PKSG80, a novel gene encoding a putative
RT chemokine receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Swa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Expressed in pituitary tissue. Not detected in
CC -!- TISSUE SPECIFICITY: Expressed in pituitary tissue. Not detected in
CC frontal, temporal and occipital lobes of the cortex, basal
CC forebrain, caudate nucleus, nucleus accumbens, and hippocampus.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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DR EMBL; AF411110; AAL26481.1; -
DR EMBL; AB083631; BAB89344.1; -
DR EMBL; AF345568; AAK29071.1; -
DR EMBL; AB065866; BAC06084.1; -
DR GenBank; HGNC:4532; GPR81.
DR MIM; 606923; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOODPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 42 1 (POTENTIAL).
FT DOMAIN 43 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 70 2 (POTENTIAL).
FT DOMAIN 71 89 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 90 110 3 (POTENTIAL).
FT DOMAIN 111 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 151 4 (POTENTIAL).
FT DOMAIN 152 182 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 183 203 5 (POTENTIAL).
FT DOMAIN 204 220 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 221 241 6 (POTENTIAL).
FT DOMAIN 242 261 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 262 281 7 (POTENTIAL).
FT DOMAIN 282 346 CYTOPLASMIC (POTENTIAL).
FT DISULFID 88 165 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 346 AA; 39295 MW; 80DB114EEB3A47A5 CRC64;

Query Match 100.0%; Score 1853; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1e-125;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCRIEDTTSQVNPPLLIIVAFVLGALGNGVALGCGFHKMTKPSIVILFNLA 60
Db 1 MYNGSCRIEDTTSQVNPPLLIIVAFVLGALGNGVALGCGFHKMTKPSIVILFNLA 60
QY 61 DELIMICLPRTDYLRHRRHAFGDIICRVGLFTLMMRAGSIYVLTVAAADRYKVVHP 120
Db 61 DELIMICLPRTDYLRHRRHAFGDIICRVGLFTLMMRAGSIYVLTVAAADRYKVVHP 120
QY 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLENHLCVQETAVSCSFIMESANGWDIM 180
Db 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLENHLCVQETAVSCSFIMESANGWDIM 180
QY 181 FOLEFFPLGLIILFCSPKIYVSLRRROQLARQARMKKATRFIMVVAIVFITCYLPVSAR 240
Db 181 FOLEFFPLGLIILFCSPKIYVSLRRROQLARQARMKKATRFIMVVAIVFITCYLPVSAR 240
QY 241 LYFLWTVPSACDPSVHGALHITLSFTYMSMLDPLVYFSSPFPKYNKIKCSLKPK 300
Db 241 LYFLWTVPSACDPSVHGALHITLSFTYMSMLDPLVYFSSPFPKYNKIKCSLKPK 300
QY 301 QPGHKTQRPPEMPSINLGRSCISVANSTFQSDGQWDPHIVEWH 346
Db 301 QPGHKTQRPPEMPSINLGRSCISVANSTFQSDGQWDPHIVEWH 346

RESULT 2
GP81_MOUSE STANDARD; PRT; 343 AA.
AC Q8C131;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable G protein-coupled receptor GPR81.
GN GPR81.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Reid J.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura K., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Orphan receptor.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
DR MGD; AK029064; BAC26273.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOODPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 42 1 (POTENTIAL).
FT DOMAIN 43 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 70 2 (POTENTIAL).
FT DOMAIN 71 90 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 91 111 3 (POTENTIAL).
FT DOMAIN 112 131 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 132 152 4 (POTENTIAL).
FT DOMAIN 153 182 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 183 203 5 (POTENTIAL).
FT DOMAIN 204 220 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 221 241 6 (POTENTIAL).
FT DOMAIN 242 259 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 260 280 7 (POTENTIAL).
FT DOMAIN 281 343 CYTOPLASMIC (POTENTIAL).
FT DISULFID 88 165 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 343 AA; 38927 MW; 917FA9499B2E03FD CRC64;

Query Match 80.0%; Score 1483; DB 1; Length 343;

```

Best Local Similarity 81.4%; Pred. No. 2.8e-99;  
Matches 276; Conservative 19; Mismatches 44; Indels 0; Gaps 0;

QY 1 MYNGSCRRLEGDTISQVMPPLIVAFVILGALGVGVALCGFCFHMKTWKSTVYLFNLAVA 60  
Db 1 MONGSCCLLEGPEISQVMPPLIVAFVILGALGVGVALCGFCFHMKTWKSTVYLFNLAVA 60

QY 61 DFLMCLPFRDYYLRRRHAFGDI PCRVGLFTLAMNAGSI VFLTVVAADRYFKVWHP 120  
Db 61 DFLMCLPFRDYYLRRRHAFGDI PCRVGLFTLAMNAGSI VFLTVVAADRYFKVWHP 120

QY 121 HAVNTISTRVAGIVCTLWALVILGTVYLLNHLVCQVETAVSCSFIMESANGHWDIM 180  
Db 121 HMVNAISNRATAACVLTWVILGTVYLLNHLVCQVETAVSCSFIMESANGHWDIM 180

QY 181 FOLEFMPGLIILFCSEFKIVWSLRQQARQAKKATRFIMVVAIVITCYLPSVSAR 240  
Db 181 FOLEFMPGLIILFCSEFKIVWSLRQQARQAKKATRFIMVVAIVITCYLPSVSAR 240

QY 241 LYELMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSFPKFKYKIKICSILKPK 300  
Db 241 LYELMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSFPKFKYKIKICSILKPK 300

QY 301 QPGHKTQRPBEMPISNLGRSCISVANSFQSDGQWD 339  
Db 301 QPGHKTQRPBEMPISNLGRSCISVANSFQSDGQWD 339

RESULT 3  
HM74\_HUMAN  
ID HM74\_HUMAN STANDARD; PRT; 387 AA.  
AC P49019;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable G protein-coupled receptor HM74.  
GN HM74.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Monocytes;  
RX MEDLINE=94092629; PubMed=7505609;  
RA Nomura H., Nielsen B.W., Matsushima K.;  
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative  
leukocyte chemotactic peptide receptors.";  
RL Int. Immunol. 5:1239-1249(1993).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
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CC -----  
DR EMBL; D10923; BAA01721.1; -;  
DR F01; I69202; I69202.  
DR HSSP; P34996; 1DDD.  
DR MIM; 606039; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00027; GPCRHHOOPS.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane.  
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 29 50 1 (POTENTIAL).  
FT DOMAIN 51 63 CYTOPLASMIC (POTENTIAL).  
FT TRANSEM 64 85 2 (POTENTIAL).  
FT DOMAIN 86 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 103 123 3 (POTENTIAL).  
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).  
FT TRANSEM 143 163 4 (POTENTIAL).  
FT DOMAIN 164 194 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 195 209 5 (POTENTIAL).  
FT DOMAIN 210 236 CYTOPLASMIC (POTENTIAL).  
FT TRANSEM 237 256 6 (POTENTIAL).  
FT DOMAIN 257 273 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 274 298 7 (POTENTIAL).  
FT DOMAIN 299 387 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 100 177 BY SIMILARITY.  
SQ SEQUENCE 387 AA; 44481 MW; C244F562C2343647 CRC64;

Query Match 47.5%; Score 880.5; DB 1; Length 387;  
Best Local Similarity 52.2%; Pred. No. 3.8e-56;  
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCRIEGDTISQVMPPLIVAFVILGALGVGVALCGFCFHMKTWKSTVYLFNLAVADPFL 64  
Db 17 NCCVFRDDPIAKVLPVILGELFIFGLLGNGLALWIFCFHLKSNKSSIFLNLAVADPFL 76

QY 65 MICLPRTDYLRHWAAGDIPCRVGLFTLAMNAGSI VFLTVVAADRYFKVWHPHVA 124  
Db 77 IICLPFMDYVYRRSDWNGDIPCRVLFMFAMNRQSIIFLTVAADRYFKVWHPHVA 136

QY 125 NTISTVAAAGIVCTLWALVILGTVYLLNHLVCQVETAVSCSFIMESANGHWDIMFQLE 184  
Db 137 NKISNNTAAIISCLLWITVGLTVHLLKKLLQNGPANVCISFSICHTFRHMAEFLE 196

QY 185 FFWPLGIILFCSEFKIVWSLRQQARQAKKATRFIMVVAIVITCYLPSVSARLYEL 244  
Db 197 FLLPLGIILFCSEFKIVWSLRQQARQAKKATRFIMVVAIVITCYLPSVSARLYEL 255

QY 245 WTVPSA----CD--PSVHGALHITLSTYMNMLDPLVYFSSFPKFKYKIKICSILKPK 299  
Db 256 WLLHTSGTQNCVYRSVDLAFFITLSTYMNMLDPLVYFSSFPKFKYKIKICSILKPK 315

QY 300 KQPGHKTQRPBEMPISNLGRSCISVANSFQSDGQWD 340  
Db 316 KATGEDNNRSTVELTGDPNKT-RGAPEALMANGEPWSP 355

RESULT 4  
GP31\_HUMAN  
ID GP31\_HUMAN STANDARD; PRT; 319 AA.  
AC O00270;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable G protein-coupled receptor GPR31.  
GN GPR31.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=97349123; PubMed=9205127;  
RA Zingoni A., Rocchi M., Storlazzi C.T., Bernardini G., Santoni A.,  
RA Napolitano M.;  
RT "Isolation and chromosomal localization of GPR31, a human gene  
encoding a putative G protein-coupled receptor.";  
RL Genomics 42:519-523(1997).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.



Db 66 TSDFLFIPTLPFRADYFRGNSWIFGDLACVMSYSLVNMYSIYFLTLVLSVVRQATV 125  
QY 119 HPHAVNTTSTRVAGIVCTLHALVILGTVYLLLENHLVCQETAVSC-----ESPIMESA 173  
D5 126 HPRFMFVT-SVR-SAWILGCIWTFMAGSALLVNGQBEKONIISCLSLSPQKF--KSL 182  
QY 174 KGWHDIMEQLEFFMPLGIILFCSPKTIWGLRRQ--QLARQARKKATRFIMVAIVEIT 231  
D5 183 LHMHLAVAGLLPLLTITVCLLIRLLKARIPESFRAHRAKALTIVIAMITPLL 242  
QY 232 CYLPSVARKLYFWTPSSACDPSVHGALHTLSFTYMSMLDPLVYFSSPSF 285  
D5 243 CELPYHALRTLHLVTWDKSCGDLHKATVITLMAAASCNCFPPYYFAGENF 296

RESULT 6  
CLNT2\_HUMAN  
ID CLNT2\_HUMAN STANDARD; PRT; 346 AA.  
AC Q9NS75; Q9HCQ2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321) (hGPCR21).  
GN CysLTR2 OR CysLTR2 OR CysLTR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=20374466; PubMed=10913337;  
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T., Nishikawa T., Kawai Y., Maehou Y., Isogai T., Suzuki Y., Sugano S., Furuichi K.;  
RT "The molecular characterization and tissue distribution of the human cysteinyl leukotriene CysLTR2 receptor."  
RL Biochem. Biophys. Res. Commun. 274:316-322 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20459128; PubMed=10851239;  
RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T., Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R., Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N., Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M., Lynch K.R., Evans J.F.;  
RT "Characterization of the human cysteinyl leukotriene 2 receptor."  
RL J. Biol. Chem. 275:30531-30536 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20545741; PubMed=11093801;  
RA Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S., Civelli O.;  
RT "Molecular cloning and characterization of a second human cysteinyl leukotriene receptor: discovery of a subtype selective agonist."  
RL Mol. Pharmacol. 58:1601-1608 (2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
Dunn M.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22040266; PubMed=12044878;  
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;  
RT "Identification of G protein-coupled receptor genes from the human genome sequence."  
RL FEBS Lett. 520:97-101 (2002).  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RU Submitter (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 17-346 FROM N.A.  
RA Suga H.;  
RT "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; AB038269; BAB03601.1; -  
CC EMBL; AF254664; AAG17281.1; -  
CC EMBL; AF279611; AAK69485.1; -  
CC EMBL; AL137118; CAC23102.1; -  
CC EMBL; AB083603; BAB89316.1; -  
CC EMBL; AY389504; AAQ91330.1; -  
CC EMBL; AB041644; BAB16379.1; -  
CC Genbank; HGNC:18274; CysLTR2.  
CC MIM; 605666;  
CC GO; GO:0004974; F:leukotriene receptor activity; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR004071; Cysleuk receptor.  
CC InterPro; IPR00276; GPCR\_Rhodopsn.  
CC Pfam; PF00001; 7tm 1; 1.  
CC PRINTS; PR01533; CysLTRSCPTR.  
CC PRINTS; PR00237; GPCR\_Rhodopsn.  
CC PROSITE; PS00237; G-PROTEIN RECP F1\_1; FALSE\_NEG.  
CC PROSITE; PS0262; G-PROTEIN RECP F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
KW DOMAIN 1 42  
FT TRANSMEM 43 63  
FT DOMAIN 64 72  
FT TRANSMEM 73 93  
FT DOMAIN 94 123  
FT TRANSMEM 124 144  
FT DOMAIN 145 153  
FT TRANSMEM 154 174  
FT DOMAIN 175 204  
FT TRANSMEM 205 225  
FT DOMAIN 226 245  
FT TRANSMEM 246 266  
FT DOMAIN 267 286  
FT TRANSMEM 287 307  
FT DOMAIN 308 346  
FT DISULFID 111 187  
FT CARBOHYD 20 20  
FT CARBOHYD 26 26  
FT CARBOHYD 30 30  
FT CARBOHYD 181 181  
SQ SEQUENCE 346 AA; 39635 MW; B554A4A2DDC5EE4 CRC64;  
Query Match 19.8%; Score 366.5; DB 1; Length 346;  
Best Local Similarity 29.9%; Pred. No. 1.9e-19;  
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;



QY 3 NGSCRIEGETISQVMPPLLIIVAFVLGALNGVALCGCFEHMKWKPKST---VYLFLNLA 59  
 Db 27 NSRNTCTE-NFKREFFPIVLIIFWGLNGLSIYF--LQPYKXSTSVNFMNLIAI 82  
 QY 60 ADFLMLICLPRTDYLRHRRHARGDIPCRVGLFTLANNRAGSIVFLTWAAADRYFKVWH 119  
 Db 83 SDLLFISTLPFRADYLRGNSWIFGELACRIMSYSLYNNYSSIVFLTVLSVRELAWVH 142  
 QY 120 PHAVNTISTVAAGIVCTLWALVILGVYVLLLENHLCVQTAVSC---ESFIMESANGW 176  
 Db 143 PFRLLHVTISR-SANILGCIITWILMASSIMLDGSGEQSGVTSCLNLYKIAKLQTM 201  
 QY 177 HDIMFOLEFFMPLGILFCSEKIVWSLRRRO--QLARQARKKATRTFMVAIVFICTYL 234  
 Db 202 NYIALVVGCLLPFTLSICYLIIIRVLKVPESGLRVSHKKAUTIIITLIIFFLCFL 261  
 QY 235 PSVSARYFLWTVPSSACDPSVHGALHITLSFTYMNMLDPLVYFSSFPKFNKLI 294  
 Db 262 PYHLRTVHLTTWKVGLCKDLRHLKALVITLALAAANACFNELLYVFAGENFK--DRUK- 317  
 QY 295 CSLKPKQGHSKTK 308  
 Db 318 SALRKGHPQAKTK 331

## RESULT 7

P2YR CHICK  
 ID P2YR CHICK STANDARD; PRT; 362 AA.  
 AC P3496;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE P2Y purinoreceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).  
 GN P2RY1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=93285340; PubMed=8508924;  
 RA Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,  
 RA King B.F., Burnstock G., Barnard E.A.;  
 RT "Cloning and functional expression of a brain G-protein-coupled ATP  
 RT receptor.";  
 RL FEBS Lett. 324:219-225 (1993).  
 RN (2)

3D-STRUCTURE MODELING.  
 RP MEDLINE=97026278; PubMed=8872457;  
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;  
 RT "Modelling the P2Y purinoreceptor using rhodopsin as template.";  
 RL Drug Des. Discov. 13:133-140 (1995).  
 CC -1- FUNCTION: Receptor for extracellular adenine nucleotides such as  
 CC ATP and ADP. Seems to mediate its action via a pertussis toxin  
 CC insensitive G-protein, probably belonging to the Gq family that  
 CC activate a phosphatidylinositol-calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Brain, spinal cord, gastrointestinal tract,  
 CC spleen and leg muscle. Is not detected in the heart, liver,  
 CC stomach, lung and kidney.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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EMBL; X73268; CAA51716.1; -.

DR PIR: S33733; S33733.  
 DR PDB: 1DDD; 11-JUL-96.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPS.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.  
 FT DOMAIN 1 41  
 FT TRANSMEM 42 63  
 FT DOMAIN 64 76  
 FT TRANSMEM 77 98  
 FT DOMAIN 99 115  
 FT TRANSMEM 116 136  
 FT DOMAIN 137 155  
 FT TRANSMEM 156 177  
 FT DOMAIN 178 207  
 FT TRANSMEM 208 227  
 FT DOMAIN 228 254  
 FT TRANSMEM 255 274  
 FT DOMAIN 275 292  
 FT TRANSMEM 293 317  
 FT DOMAIN 318 362  
 FT DISULFID 113 191  
 FT CARBOHYD 11 11  
 FT CARBOHYD 26 26  
 FT CARBOHYD 102 102  
 FT CARBOHYD 186 186  
 FT HELIX 42 69  
 FT HELIX 77 102  
 FT HELIX 115 137  
 FT HELIX 154 178  
 FT HELIX 205 231  
 FT HELIX 250 275  
 FT HELIX 290 305  
 FT TURN 306 307  
 FT HELIX 308 320  
 SQ SEQUENCE 362 AA; 41194 MW; A806C88EB9514761 CRC64;

Query Match 19.6%; Score 364; DB 1; Length 362;

Best Local Similarity 29.1%; Pred. No. 3e-19;

Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPPLIIVAFVLGALNGVALCGCFEHMKWKPKSTVYLNLAADRYFKVWH 77

Db 43 LPVYILVFIITGELGNSVAILWFMVFNRPMSGISVYMFNLALADFLVYLLPALIFYFN 102

QY 78 RRHWAFGDIPCRVGLFTLANNRAGSIVFLTWAAADRYFKVWHPHAVNTISTRVAAGIVC 137

Db 103 KTDWIFGDVNMCKLQRFIFHVNLYGSLFLTCISVHRVTGVVHPLKSLGRLKKNAVYSS 162

QY 138 TLVALVYL-----GTVYLLLENHLCVQETA-----VSCSFIMESANGWHD 178

Db 163 LVNALVAVIATPIILFYSGTGVRNRKTIICYDTTADERYLSFYVSMCTTVFM----- 214

QY 179 IMQLGEFFMPLGILFCSEKIVWSLRRROQLARQARKKATRTFMVAIVFICTYLP--- 235

Db 215 -----FCIPFIVILGCGYGLIVKALYK-DLDSPLRKRKSIYVILVTFVAVSYLPHV 267

QY 236 -----SVSARYFLWTVPSSACDPSVHGALHITLSFTYMNMLDPLVYFSSFPKFNK 291

Db 268 MKTLNLRARLDF-QTPQMCANFNDKVATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR 326

QY 292 LKICSLKPKQGHSKTKQRPPEMPSML 318

Db 327 ATRKSRSEP--NVQSKSEMTNIL 351

## RESULT 8

P2YR MELGA

ID P2YR MELGA STANDARD; PRT; 362 AA.

AC P49652;

DT 01-FEB-1996 (Rel. 33, Created)



## RESULT 10

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RESULT 11
P2YR_RAT
ID P2YR_RAT STANDARD; PRT; 373 AA.
AC P49651;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2YR1.
OS Rattus norvegicus [Rat].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP P2YR_RAT
RX MEDLINE=95298025; PubMed=7779087;
RA Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT "Cloning of rat and mouse P2Y purinoceptors";
RL Biochem. Biophys. Res. Commun. 211:211-218(1995).
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP. In pancreatic islets, may mediate some of the effects
CC of extracellular ATP on insulin secretion.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in muscle, heart, liver, kidney,
CC lung, brain, spleen, but not in testis.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U22830; AAA91303.1; --
CC HSPSP: P34996; 1DD
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCRHOPOSPN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42321 MW; 6DDF676287B5E648 CRC64;

Query Match 19.3%; Score 358.5; DB 1; Length 373;
Best Local Similarity 27.0%; Pred. No. 7.6e-19;
Matches 91; Conservative 68; Mismatches 139; Indels 39; Gaps 8;

QY 18 MPPLLIIVAFVLGALNGVALCGCFHMKWKPSTVILFNLAVADFLLMLICLPFRDYVLR 77

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Db 54 LPNAVILVFIIGLNSVAIWMFVFMKPSGISVTFNLADEFLVTLPLIFYYEN 113
QY 78 RHNWAFGDI PCRVGLFTLAMNRAGSIVFTVVAADRYFKVPHPHAVNTISTVAAGIVC 137
Db 114 KTDWTFGDMVKLQRFIFHNLVGLSILFTCSAHRYSGVWVYELKSLGRLKKNVIVSV 173
QY 138 TIALWLVILGTVVLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFEM 187
Db 174 LVNLIVVVAISPILFYSGTGIRKNTVTCTYDSTSDYLSRYFSYM-----CTTVAMFCI 228
QY 188 PLGILFSCFKIWMGLRRQQLARQARMKATRFMVAIVFITCYLP-----SVSAR 240
Db 229 FLVILIGCVGLVRLAIYK-DLDNSPLRKSYIVLIVITVFAVSIPPHVMTNMLRAR 287
QY 241 LYFLMTVPSSACD--PSVGHALHITLSFTYMSMLDPLVYFSSPFPKPKNKIKICSLK 298
Db 288 LDF---QTPMCDENDRVVATYQVTRGLASLNSCVDPILYFLAGDTFRRLSLR----- 337
QY 299 PKQPGHSHKTQRPPEMPISNLGRSCISVANSFQSQSD 335
Db 338 ----ATRKASRRSEANLQSKSEMTINILSEFKQNGD 370

RESULT 12
P2YR_CAVPO
ID P2YR_CAVPO STANDARD; PRT; 373 AA.
AC P59902;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2YR1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Hartley; TISSUE=small intestine;
RA Gao N., Hu H., Zhu M.X., Wood J.D.;
RA "A novel P2Y1 receptor in the guinea pig submucous plexus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for extracellular adenine nucleotides such as
CC ATP and ADP (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY048684; AAL05953.1; --
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 58 78
FT DOMAIN 79 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 90 110
FT DOMAIN 111 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149
FT DOMAIN 150 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 188
FT DOMAIN 189 220
FT TRANSMEM 221 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 258
FT TRANSMEM 259 279
FT DOMAIN 280 310 EXTRACELLULAR (POTENTIAL).

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 17:18:53 ; Search time 45 Seconds  
(without alignments)  
2425.984 Million cell updates/sec

Title: US-10-076-260-2  
Perfect score: 1853  
Sequence: 1 MYNSCCRIEGDTISQVMP .....ANSFQSGQWDPHIVWH 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	883.5	47.7	363	4 Q8TDS4	Q8TDS4 homo sapien
2	881.5	47.6	387	4 Q8NGE4	Q8NGE4 homo sapien
3	868.5	46.9	360	11 Q9EP66	Q9EP66 mus musculus
4	862.5	46.5	360	11 Q80Z39	Q80Z39 rattus norv
5	596	32.2	283	4 Q8NGV8	Q8NGV8 homo sapien
6	529	28.5	384	4 Q8NGW4	Q8NGW4 homo sapien
7	529	28.5	384	4 Q86WP7	Q86WP7 homo sapien
8	529	28.5	423	4 Q8TDS5	Q8TDS5 homo sapien
9	450.5	24.3	319	4 Q9NQ20	Q9NQ20 homo sapien
10	446.5	24.1	319	11 Q9JLS1	Q9JLS1 mus musculus
11	375.5	20.3	309	11 Q8K528	Q8K528 mus musculus
12	351.5	19.0	390	13 Q8GQ4	Q8GQ4 carassius a
13	348.5	18.8	373	11 Q8BMJ5	Q8BMJ5 mus musculus
14	342.5	18.5	357	13 Q9DE05	Q9DE05 raja erinac
15	341	18.4	361	13 Q90X57	Q90X57 xenopus lae
16	340.5	18.4	370	11 Q8BKK1	Q8BKK1 mus musculus

17	337	18.2	339	4 Q8NS57	Q8NS57 homo sapien
18	336.5	18.2	370	11 Q8BLG2	Q8BLG2 mus musculus
19	336	18.1	390	13 Q8AXM7	Q8AXM7 carassius a
20	330	17.8	347	13 Q7ZZA4	Q7ZZA4 brachydanio
21	329.5	17.8	380	13 Q9DGO6	Q9DGO6 carassius a
22	325	17.5	309	4 Q86UH4	Q86UH4 homo sapien
23	325	17.5	344	4 Q7Z380	Q7Z380 homo sapien
24	323.5	17.5	344	4 Q7Z386	Q7Z386 homo sapien
25	317.5	17.1	377	13 Q7T2S9	Q7T2S9 carassius a
26	316	17.1	407	13 Q8JID5	Q8JID5 carassius a
27	309.5	16.7	307	11 Q8BS98	Q8BS98 mus musculus
28	308.5	16.6	307	11 Q8CB97	Q8CB97 mus musculus
29	307	16.6	337	4 Q8IV19	Q8IV19 homo sapien
30	303.5	16.4	359	6 Q9NOU1	Q9NOU1 ovis aries
31	301	16.2	365	11 Q8EQ97	Q8EQ97 mus musculus
32	300.5	16.2	346	6 Q9SKS6	Q9SKS6 ovis aries
33	300	16.2	367	6 Q8MI04	Q8MI04 ovis aries
34	298.5	16.1	385	4 Q86YF2	Q86YF2 homo sapien
35	298	16.1	375	11 Q8BY11	Q8BY11 mus musculus
36	297	16.0	370	13 Q8UWL5	Q8UWL5 fugu rubrip
37	297	16.0	390	11 Q7T186	Q7T186 rattus norv
38	297	16.0	399	11 Q8R311	Q8R311 mus musculus
39	293	15.8	315	6 Q9GKP7	Q9GKP7 sus scrofa
40	293	15.8	374	13 Q57466	Q57466 meleagris g
41	293	15.8	385	11 Q9TK40	Q9TK40 mus musculus
42	292.5	15.8	361	6 Q46685	Q46685 bos taurus
43	292	15.8	317	11 Q99MT6	Q99MT6 mus musculus
44	292	15.8	359	6 Q9GLN9	Q9GLN9 pan troglod
45	291	15.7	359	11 Q9EPP3	Q9EPP3 cavia porce

#### ALIGNMENTS

#### RESULT 1

Q8TDS4 ID Q8TDS4 PRELIMINARY; PRT; 363 AA.  
AC Q8TDS4;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Putative G-protein coupled receptor (Seven transmembrane helix receptor).  
GN GPCR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;  
RT "Identification of G protein-coupled receptor genes from the human genome sequence.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;  
RT "Genome-wide discovery and analysis of human seven transmembrane helix receptor genes.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=22513958; PubMed=12522134;  
RA Wise A., Ford S.M., Fraser N.J., Barnes A.A., Elshourbagy N., Eilert M., Ignar D.M., Murdock P.R., Steplewski K., Green A., Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H., Wilson S., Pike N.B.;  
RT "Molecular Identification of High and Low Affinity Receptors for Nicotinic Acid.";  
RL J. Biol. Chem. 278:9869-9874 (2003).  
RN [4]  
RP SEQUENCE FROM N.A.

RA Elshourbagy N.A.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AB083632; BAB89345.1; -.  
 DR EMBL; AB065876; BAC06094.1; -.  
 DR EMBL; AY148884; AAN71621.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 363 AA; 41849 MW; C4B0EEC9CCB81D56 CRC64;

Query Match 47.7%; Score 883.5; DB 4; Length 363;  
 Best Local Similarity 52.8%; Pred. No. 4.6e-78;  
 Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCRIEGETISQVMPPLIIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 64  
 Db 17 NCCVFRDDEFIKVLPEVLGLEPIFGLLGNGLALWIFCFHLKSKSSRIFLFNLAVADFL 76  
 QY 65 MICLPFRDYLLRRRHWAFGDIPCRVGLFTLANNRAGSVFVTVAAADRYKVVVPHAV 124  
 Db 77 IICLPFMDNYVRRDWFPGDIPCRVLVLFNFPANNRQGSIIFTVVAADRYFVVVPHAL 136  
 QY 125 NTISTRVAAGIVCTILWALVILGTVYLLLENHLVCQETAVSCSFIMESANGWHDIMFOLE 184  
 Db 137 NKISNRTAIIISCLLWGITVGLTVHLLKKLLIQNGPANVCISFSICHTFRHGANFLE 196  
 QY 185 FPMPLGIILFCSEKIVSIRRRQOLARQMKKATRFIMVAIVFITCYLPSVSARLYFL 244  
 Db 197 FFLPLGIILFCSARIISLRQ- QMDRAKIKRAITFMVAIVFVFCPLPSVVVRIRIF 255  
 QY 245 WTVPSA---CD--PSVHGALHITLSFTYMSMLDPLVYFSSPSPKPKYKIKICSLKP 299  
 Db 256 WLLHTSGTQNCVRSVDLAPFITLSFTYMSMLDPLVYFSSPSPFPNFFSLINRCLQR 315  
 QY 300 KQPGHKTQRPPEMIPISNLGRSCISVANSFOSQSDGQWDP 340  
 Db 316 KVTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEWSP 355

RESULT 2  
 Q8NGS4 Q8NGE4 PRELIMINARY; PRT; 387 AA.  
 AC Q8NGE4;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Seven transmembrane helix receptor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,  
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.  
 RT "Genome-wide discovery and analysis of human seven transmembrane helix  
 RT receptor genes".  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB065865; BAC06083.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.

DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW Receptor; Transmembrane.  
 SQ SEQUENCE 387 AA; 44495 MW; 26433C8558E5EC81 CRC64;

Query Match 47.6%; Score 881.5; DB 4; Length 387;  
 Best Local Similarity 52.2%; Pred. No. 7.7e-78;  
 Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCRIEGETISQVMPPLIIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 64  
 Db 17 NCCVFRDDEFIKVLPEVLGLEPIFGLLGNGLALWIFCFHLKSKSSRIFLFNLAVADFL 76  
 QY 65 MICLPFRDYLLRRRHWAFGDIPCRVGLFTLANNRAGSVFVTVAAADRYKVVVPHAV 124  
 Db 77 IICLPFMDNYVRRDWFPGDIPCRVLVLFNFPANNRQGSIIFTVVAADRYFVVVPHAL 136  
 QY 125 NTISTRVAAGIVCTILWALVILGTVYLLLENHLVCQETAVSCSFIMESANGWHDIMFOLE 184  
 Db 137 NKISNRTAIIISCLLWGITVGLTVHLLKKLLIQNGPANVCISFSICHTFRHGANFLE 196  
 QY 185 FPMPLGIILFCSEKIVSIRRRQOLARQMKKATRFIMVAIVFITCYLPSVSARLYFL 244  
 Db 197 FFLPLGIILFCSARIISLRQ- QMDRAKIKRAITFMVAIVFVFCPLPSVVVRIRIF 255  
 QY 245 WTVPSA---CD--PSVHGALHITLSFTYMSMLDPLVYFSSPSPKPKYKIKICSLKP 299  
 Db 256 WLLHTSGTQNCVRSVDLAPFITLSFTYMSMLDPLVYFSSPSPFPNFFSLINRCLQR 315  
 QY 300 KQPGHKTQRPPEMIPISNLGRSCISVANSFOSQSDGQWDP 340  
 Db 316 KVTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEWSP 355

RESULT 3  
 Q3EP66 Q3EP66 PRELIMINARY; PRT; 360 AA.  
 AC Q3EP66;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Putative seven transmembrane spanning receptor.  
 GN PUMAG OR POMA-G.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ, and C57BL/6;  
 RA Schaub A., Futterer A., Pfeiffer K.;  
 RT "POMA-G, an interferon-gamma inducible gene in macrophages is a novel  
 RT member of the seven transmembrane spanning superfamily".  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL; AJ300199; CAC17791.1; -.  
 DR EMBL; AJ300198; CAC17790.1; -.  
 DR MGD; MGI:1933383; Pumag.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005525; F:GTP binding; IEA.  
 DR GO; GO:0001614; F:purinergic nucleotide receptor activity; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 360 AA; 41400 MW; CCCE52A2475777FC CRC64;

Query Match 46.9%; Score 868.5; DB 11; Length 360;

Best Local Similarity 55.6%; Pred. No. 1.3e-76; Matches 178; Conservative 39; Mismatches 96; Indels 7; Gaps 4;									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
RESULT 4									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 46.5%; Score 862.5; DB 11; Length 360; Best Local Similarity 54.7%; Pred. No. 5.2e-76; Matches 175; Conservative 43; Mismatches 95; Indels 7; Gaps 4;									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 32.2%; Score 596; DB 4; Length 263; Best Local Similarity 59.9%; Pred. No. 4.5e-50; Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;									
QY	5	SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	64
Db	17	NCCVPRDDP	FIVK	VPVGL	EPFGL	GLNGLALWIF	CFHLKSWK	SRIFL	76
QY	65	MLCLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	124
Db	77	ICLPLFMDN	YVVRWD	WKF	GDPIC	RLMLF	MLANNRQGS	IFL	136
QY	125	NTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	184
Db	137	NKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	196
QY	185	FMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	197	FELPLGLILFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
RESULT 6									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 32.2%; Score 596; DB 4; Length 263; Best Local Similarity 59.9%; Pred. No. 4.5e-50; Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;									
QY	5	SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	64
Db	17	NCCVPRDDP	FIVK	VPVGL	EPFGL	GLNGLALWIF	CFHLKSWK	SRIFL	76
QY	65	MLCLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	124
Db	77	ICLPLFMDN	YVVRWD	WKF	GDPIC	RLMLF	MLANNRQGS	IFL	136
QY	125	NTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	184
Db	137	NKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	196
QY	185	FMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	197	FELPLGLILFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
RESULT 6									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 32.2%; Score 596; DB 4; Length 263; Best Local Similarity 59.9%; Pred. No. 4.5e-50; Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;									
QY	5	SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	64
Db	17	NCCVPRDDP	FIVK	VPVGL	EPFGL	GLNGLALWIF	CFHLKSWK	SRIFL	76
QY	65	MLCLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	124
Db	77	ICLPLFMDN	YVVRWD	WKF	GDPIC	RLMLF	MLANNRQGS	IFL	136
QY	125	NTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	184
Db	137	NKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	196
QY	185	FMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	197	FELPLGLILFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
RESULT 6									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 32.2%; Score 596; DB 4; Length 263; Best Local Similarity 59.9%; Pred. No. 4.5e-50; Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;									
QY	5	SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	64
Db	17	NCCVPRDDP	FIVK	VPVGL	EPFGL	GLNGLALWIF	CFHLKSWK	SRIFL	76
QY	65	MLCLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	124
Db	77	ICLPLFMDN	YVVRWD	WKF	GDPIC	RLMLF	MLANNRQGS	IFL	136
QY	125	NTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	184
Db	137	NKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	196
QY	185	FMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	197	FELPLGLILFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
RESULT 6									
QY	3	NG-SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	61
Db	11	NGKNCVFRDENIAKVLPP	VIGLEFV	GLNGLALWIF	CFHLKSWK	SRIFL	FNLA	VAD	70
QY	62	FLMICLPFRDYLRERRHAF	GDI	PCRVGL	FTLANNRAGS	IVFL	TVAA	DRYFKV	121
Db	71	FLMICLPFLTDNYVHND	WRFGI	PCRVML	FMLANNRQGS	IFL	TVAA	DRYFRV	130
QY	122	HAVNTISTRVAGIVCT	LMALVIL	GTGYLL	LENHL	CVQETAV	SCBSF	IMESANG	181
Db	131	HFLNKISNRTAAIS	CLWGLT	GLTVHLLY	TNNMTK	GEAL	YLCSS	FSICYN	190
QY	182	OLEFFMPLGLILFC	SPKIV	WSRRQ	LAQARM	KKAT	RFIM	VAIF	241
Db	191	LLEFFLPLAIIIFC	SGRII	WSLRQ	-QMDRHV	KIKRA	IN	FMVA	249
QY	242	YFLWTVP	---	SACD	--PSVHG	ALHIT	LSFTY	NNMLD	296
Db	250	RIFWLLYKYN	RNC	DISSV	DLA	FFTL	SFTY	NNMLD	309
QY	297	LKPQKQCHSK	TQRP	EMPIS	316				
Db	310	LRRKTLGEP	DN	NRST	SVELT	329			
Query Match 32.2%; Score 596; DB 4; Length 263; Best Local Similarity 59.9%; Pred. No. 4.5e-50; Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;									
QY	5	SCRIEGDTISQVMPPLII	VAFLV	GALNGVALCGFC	CHMTWKPS	TVYLF	FNLA	VAD	64
Db	17	NCCVPRDDP	FIVK	VPVGL	EPFGL	GLNGLALWIF	CFHLKSWK	SRIFL	76
QY	65	MLCLPFRDYLRERRHAF	GDI	PCRVGL					

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsuchumi S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065652; BAC05878.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 384 AA; 41426 MW; 1C8455FED8085F36 CRC64;

Query Match 28.5%; Score 529; DB 4; Length 384;
Best Local Similarity 39.2%; Pred. No. 2.4e-43;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

QY 4 GSCCRIGDTISQVMPPLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
DB 42 GPCHTSSLSVSAFAFLAPILALEFVLGNGSLALFICHTPTWNTVFLVSLVAADFL 101
QY 64 LMICLPFTDYLLRRRHAFGDPICRVGLFTLAMNAGSIVELTVVADRYKVVHPHHA 123
DB 102 LISNPLRVDDYLLHETWRFGAACKVNFMLSTRTASVFLTALANRYLKVVQPHV 161
QY 124 VNTISTRVAAGIVCTIMALVILGTVYLLENHLCVQE-TAVSCSEFIM----ESANGMHD 178
DB 162 LSRASVGAARVAGGLWGI-----LLNGHLLSTFGSPCLSYRVGTPKPSASLRHQ 215
QY 179 IMFOLPEFMPGLIILFCSPKIVWSRRRQOLARQARKMKATFIMVAIVFTICVLPVS- 237
DB 216 ALYLLEFFLPALILFAIVSIGLTIRNR-GLGQAGQPORAMRVAMVAVYTCFLPSII 274
QY 238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMSMLDPLVYFSSPSF 285
DB 275 FGMASVAFWLSACKSLDCTQLFHG----SLAFTYLSVLDPLVLYCFSSPNF 323

RESULT 7
Q86WP7 PRELIMINARY; PRT; 384 AA.
AC Q86WP7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative 5-oxo-ETE G-protein coupled receptor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jones C.E., Holden S., Tennant L., Bhatia U., Suwen K., Tranter P.,
RA Turner J., Kettle R., Bouhelal R., Charlton S., Nirmala N., Jarai G.,
RA Finan P.;
RT "Expression and Characterization of a 5-oxo-ETE Receptor Highly Expressed on Human Eosinophils
RT Eicosatetraenoic Acid Receptor"

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RT and Neutrophils.";
RL Mol. Pharmacol. 63:471-477(2003).
DR EMBL; AY158687; AAC17739.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 384 AA; 41412 MW; 0C5E35FED8085F36 CRC64;

Query Match 28.5%; Score 529; DB 4; Length 384;
Best Local Similarity 39.2%; Pred. No. 2.4e-43;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

QY 4 GSCCRIGDTISQVMPPLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
DB 42 GPCHTSSLSVSAFAFLAPILALEFVLGNGSLALFICHTPTWNTVFLVSLVAADFL 101
QY 64 LMICLPFTDYLLRRRHAFGDPICRVGLFTLAMNAGSIVELTVVADRYKVVHPHHA 123
DB 102 LISNPLRVDDYLLHETWRFGAACKVNFMLSTRTASVFLTALANRYLKVVQPHV 161
QY 124 VNTISTRVAAGIVCTIMALVILGTVYLLENHLCVQE-TAVSCSEFIM----ESANGMHD 178
DB 162 LSRASVGAARVAGGLWGI-----LLNGHLLSTFGSPCLSYRVGTPKPSASLRHQ 215
QY 179 IMFOLPEFMPGLIILFCSPKIVWSRRRQOLARQARKMKATFIMVAIVFTICVLPVS- 237
DB 216 ALYLLEFFLPALILFAIVSIGLTIRNR-GLGQAGQPORAMRVAMVAVYTCFLPSII 274
QY 238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMSMLDPLVYFSSPSF 285
DB 275 FGMASVAFWLSACKSLDCTQLFHG----SLAFTYLSVLDPLVLYCFSSPNF 323

RESULT 8
Q8TDS5 PRELIMINARY; PRT; 423 AA.
AC Q8TDS5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22191290; PubMed=12065583;
RA Hosoi T., Koguchi Y., Sugikawa E., Chikada A., Ogawa K., Tsuda N.,
RA Suto N., Tsunoda S., Taniguchi T., Ohnuki T.;
RT "Identification of a Novel Human Eicosanoid Receptor Coupled to
RT Gi/o.";
RL J. Biol. Chem. 277:31459-31465(2002).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB083630; BAB99343.1; -.
DR EMBL; AB083055; BAC11806.2; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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Db 243 VLHIFQEFKSCVQQAIRMSADISLTLCHSLTSPALYCFNSNPAFTSHYRKV-LKSLR 301
Qy 299 PKQPGHKTQRPPEMPSNL 318
Db 302 GR-----RKAESPSPNL 314

RESULT 11
Q8R528 ID Q8R528 PRELIMINARY; PRT; 309 AA.
AC Q8R528;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cysteinyln leukotriene 2 receptor.
GN CYSLTR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP "Mouse CysLT2 Gene.";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB058930; BAB6881.1; -.
DR MGJ; MGI:1917336; Cysltr2.
DR GO; GO:0031631; F:cysteinyln leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CysLTR2.
DR PROSITE; PS00237; GPCR_HODOPSIN.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC6B8AF96974 CRC64;

Query Match 20.3%; Score 375.5; DB 11; Length 309;
Best Local Similarity 32.7%; Pred. No. 2e-28;
Matches 96; Conservative 56; Mismatches 125; Indels 17; Gaps 7;

Qy 2 YNGSCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKMTWKPTST---VYLENLA 58
Db 10 YSNRNCTIE-NFKKEFPIIILIFFGALNGFSYVF---LQCKKSTVNVFMLELA 65
Qy 59 VADFLMLCLPFRITYLRRRHAFGDIPICRVGLFTLANRAGSIIVFLTVAAADRYFKV 118
Db 66 TSDPLFISTLPFRADYIFRGSNWIFGDLACRVMSYSLVNMYSIYFLTVLSVRFATV 125
Qy 119 HPHAVNTISTRVAAAGIVCTLMALVILGTVYLLNHLVCQETAVSC-----ESFIMESA 173
Db 126 HPFMEFHTSVR-SAWILCGIIVFIMASSALLVNGQEEKNTIISCLSPQKF--KSL 182
Qy 174 NGHNDIMFQLEFEMPLGLIILFCSPKIVSLRRQ--QLARQMKKATRTFMVAIVFIT 231
Db 183 LHMNHIAVAGFLDPLFTLTICVLLIIRILKAIPESSGPRAAHKALTTIVIAMITLL 242
Qy 232 CYLPSVSRILYFLTVFPSSACDPSVHGALHITLSTFTYNSMLDPLVYFFSPSP 285
Db 243 CFLPYHALRTHLTVTDKSGGVHLKATVITLTMAAANSFCNPLYYFAGENF 296

RESULT 12
Q8OQ04 ID Q8OQ04 PRELIMINARY; PRT; 390 AA.
AC Q8OQ04;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type five-like somatostatin receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Peter R.E.;
RT "Cloning and expression of a type five-like somatostatin receptor in goldfish.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF252879; AAM18905.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR001092; HLH_Basic.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44136 MW; EC12119A486CF9A8 CRC64;

Query Match 19.0%; Score 351.5; DB 13; Length 390;
Best Local Similarity 30.0%; Pred. No. 5.9e-26;
Matches 97; Conservative 71; Mismatches 134; Indels 21; Gaps 10;

Qy 3 NGSCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKMTWKPTSTVYLFNLAVDF 62
Db 30 NGSSMAEEDST--KILAVIYLVFVVGTLGNSLAIFVYLYRTYTKMTATNMYILNLAVDE 87
Qy 63 LLMICLPRTDYLLRRRHAFGDIPICRVGLFTLANRAGSIIVFLTVAAADRYFKVHPH 122
Db 88 LYILGLPFLTAHNM-LGYWPFENFLCRLIMWIDSISQTSFTFCLTVMSIDRIMAVVHPTR 146
Qy 123 AVNTISTRVAAAGIVCTLMALVILGTVYLLNHLVCQETAVSCSFIMESANGHD--IM 180
Db 147 SARWRPRVAKVINSVMVALSCLLTLPVIL--YCDVQPELNTCLNSWPEPRDVMSTAFIL 204
Qy 181 P--OLEFMPGLIILFCSPKIVNSLR---RRQOLARQARM-KKATRTFMVAIVFITCVL 234
Db 205 YTAMLGFEFFPLMWITCLCYLLIVIKVKSASAGLSKGRSEKKVTRMVIIVVFLCWL 264
Qy 235 P-SVSARLYFLTVFPSSACDPSVHGALHITLSTFTYNSMLDPLVYFFSPSPFKFNKL- 292
Db 265 PFPITINILNISTLPENSL---MTGIYFLTVILTVNSCANPLLYSLFSDNFKRSFQVQL 321
Qy 293 ---KICSLKPKQPGHKTQRPPE 312
Db 322 CIHKVGVSNHNGPGRHLSRSQ 344

RESULT 13
Q8BMJ5 ID Q8BMJ5 PRELIMINARY; PRT; 373 AA.
AC Q8BMJ5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P2Y purinoceptor 1.
GN P2RY1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The FANTOM Genome Exploration Research Group Phase I & II Team;
```





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OM protein - protein search, using sw model

Run on: June 30, 2004, 17:20:22 ; Search time 23 Seconds  
(without alignments)  
776.634 Million cell updates/sec

Title: US-10-076-260-2

Perfect score: 1853

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCUTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	881.5	47.6	387	4	US-09-170-496D-222
2	880.5	47.5	387	4	US-09-170-496D-108
3	529	28.5	423	2	US-08-955-713-2
4	510	27.5	476	2	US-08-955-713-4
5	451.5	24.4	319	3	US-09-130-749-2
6	451.5	24.4	319	3	US-09-130-749-2
7	448.5	24.2	319	4	US-09-170-496D-60
8	448.5	24.2	319	4	US-09-170-496D-196
9	371	20.0	362	3	US-08-513-974B-374
10	362.5	19.6	373	2	US-08-559-524A-4
11	362.5	19.6	373	3	US-08-749-707-4
12	362.5	19.6	373	4	US-09-947-922-4
13	361.5	19.5	346	4	US-09-585-876-2
14	346.5	18.7	370	3	US-08-781-250-2
15	336	18.1	339	1	US-08-153-848-44
16	336	18.1	339	2	US-08-812-871-3
17	336	18.1	339	3	US-09-299-843A-44
18	336	18.1	339	4	US-09-088-337B-44
19	336	18.1	339	4	US-09-170-496D-32
20	336	18.1	339	5	PCT-US93-11153-44
21	336	18.1	339	5	PCT-US95-07180-2
22	335	18.1	339	4	US-09-170-496D-182
23	328.5	17.7	302	2	US-08-467-948A-30
24	328.5	17.7	302	3	US-08-467-947A-30
25	327	17.6	309	3	US-09-422-869-20
26	325	17.5	344	2	US-08-467-948A-8
27	325	17.5	344	3	US-08-467-947A-8

28	315.5	17.0	374	4	US-09-102-710B-3	Sequence 3, Appli
29	314	16.9	373	3	US-08-513-974B-373	Sequence 373, App
30	308	16.6	325	1	US-08-118-270-51	Sequence 51, Appl
31	308	16.6	325	5	PCT-US93-08528-51	Sequence 51, Appl
32	307	16.6	391	1	US-07-816-283-4	Sequence 4, Appli
33	307	16.6	391	1	US-08-417-103-4	Sequence 4, Appli
34	307	16.6	395	1	US-08-097-938-5	Sequence 5, Appli
35	307	16.6	395	1	US-08-476-000-5	Sequence 5, Appli
36	307	16.6	395	1	US-08-472-840-5	Sequence 5, Appli
37	307	16.6	395	2	US-08-476-976-5	Sequence 5, Appli
38	307	16.6	395	3	US-08-474-410-5	Sequence 5, Appli
39	306	16.5	398	1	US-08-097-938-6	Sequence 6, Appli
40	306	16.5	398	1	US-08-476-000-6	Sequence 6, Appli
41	306	16.5	398	1	US-08-472-840-6	Sequence 6, Appli
42	306	16.5	398	2	US-08-476-976-6	Sequence 6, Appli
43	306	16.5	398	3	US-08-474-410-6	Sequence 6, Appli
44	306	16.5	398	3	US-08-486-673B-6	Sequence 6, Appli
45	305.5	16.5	369	3	US-08-120-601B-9	Sequence 9, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-170-496D-222  
; Sequence 222, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 222

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-222

Query Match	47.6%	Score 881.5;	DB 4;	Length 387;
Best Local Similarity	52.2%	Pred. No. 3.6e-68;		
Matches 178;	Conservative 49;	Mismatches 107;	Indels 7;	Gaps 4;
QY	5	SCCRIGDTISQVMPPLIIVAFVLGALNGVALCGCFHMTKTPKSTVYLFNLA	VADELL 64	
Db	17	NCCVFRDDFIKVLPPVGLGFIFGLLGNGLALWIPCFHLKSKWSRIFLFLNLA	VADELL 76	
QY	65	MICLPRTDYLRHHWAFGIPCKVGLFTLMMRAGSIVELTVVAADRYPKVHPHAAV	124	
Db	77	IICLPFYMDYVRRSDWKFGDIPCLVLFMFANRQSGIIELTVAADVRYRVVHPHAAV	136	
QY	125	NTISTRAAGVCTLMAVLIGTVYLLLENHLCVQETAVSCESPIMESANGWHDIMFOLE	184	
Db	137	NKISNTAAIISCLWGITVGLTVHLLKKLLIQNGPANVCISFISICTFTFMHAAFMFLLE	196	
QY	185	FFMPLGILFCSPKIVMSLRRLQALQARKKATRTFMVAIVFITCYLPSVSARLYEL	244	
Db	197	FLPLGLGILFCSARIILWSLQR-QMDRHAKTKRAKTIIMVAIVFICFLSVVVRIRIF	255	
QY	245	WTPVSSA---CD--PSVHGALHITLSFTYNNMMLDPLVYFESSPFKPKYKLCIKCSLKP	299	
Db	256	WLLHTSGTQNCVVRSDLAFFITLSFTYNNMMLDPLVYFESSPFKPKYKLCIKCSLKP	315	
QY	300	KQCHSKTQPEPWPISNLGRRCISVANSFQSGDQWDP	340	
Db	316	KMTGEPPNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP	355	

RESULT 2  
 US-09-170-496D-108  
 ; Sequence 108, Application US/09170496D  
 ; Patent No. 6555339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic P.  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Liaw, Chen W.  
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
 ; FILE REFERENCE: AREN-0040  
 ; CURRENT APPLICATION NUMBER: US/09/170,496D  
 ; CURRENT FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 294  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 108  
 ; LENGTH: 387  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-170-496D-108

Query Match 47.5%; Score 880.5; DB 4; Length 387;  
 Best Local Similarity 52.2%; Pred. No. 4, 4e-68;  
 Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;  
 QY 5 SCRIEGBDTSQVMPPLIIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 64  
 Db 17 NCCVFRDDFAKVLPPVGLGFIFGLLGNLALWFCFHLKSKWSRIFLNLAVADFL 76  
 QY 65 MICLPEFTDYVLRHWAAGDIPCRVGLFTLAMRAGSIVILTVVADRYKVVHPHVA 124  
 Db 77 IICLPFYNDYVRRSDWNFGDIPCRVGLFTLAMRAGSIVILTVVADRYKVVHPHVA 136  
 QY 125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFMTESANGWHDIMFGL 184  
 Db 137 NKISNWTAAIISCLLWITVGLTWHLLXKLLIQNGPANVCISICHTFFWHHEMELLE 196  
 QY 185 FFMPLGILFCSEKIVWSLRRRQQLARQARMKATRFIMVVAIVITCYLPSVSARLYFL 244  
 Db 197 FLPLGLILFCSARIINSLRQR-QMDRHAKIKRAITFIMVVAIVITCYLPSVVRIRIF 255  
 QY 245 WTVPSSA--CD--PSVHGALHITLSTYMNMLDPLVYFSSSPKFKYKLCISLKP 299  
 Db 256 WLLHSTQNCVETRSVDLAFITLSTYMNMLDPLVYFSSSPKFKYKLCISLKP 315  
 QY 300 KQPGHKTQRPPEMPISNLGRSCISVANSFQSQDQWDP 340  
 Db 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEFWSF 355

RESULT 3  
 US-08-955-713-2  
 ; Sequence 2, Application US/08955713  
 ; Patent No. 5955308  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SATHE, GANESH  
 ; APPLICANT: MOONEY, JEFFREY  
 ; APPLICANT: BERGSMAN, DEBK  
 ; APPLICANT: HALSEY, WENDY  
 ; TITLE OF INVENTION: cDNA CLONE HE0AD54 THAT ENCODES A HUMAN 7-TRANS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/955,713  
 ; FILING DATE: 23-OCT-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/050,124  
 ; FILING DATE: 18-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GH-70087  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 423 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-955-713-2

Query Match 28.5%; Score 529; DB 2; Length 423;  
 Best Local Similarity 39.2%; Pred. No. 8, 1e-38;  
 Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;  
 QY 4 GSCRIEGBDTSQVMPPLIIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63  
 Db 81 GPCHZTSSLSVSAFLAPITALEFVLGLVGNLSALFIFCIHTRPMTSNTVFLVSLVAADFL 140  
 QY 64 LMICLPEFTDYVLRHWAAGDIPCRVGLFTLAMRAGSIVILTVVADRYKVVHPHVA 123  
 Db 141 LISLPLRVYDYLHETWRFGAAAACKVNLFMLSNRTASVYVFLTAIALNRYLKVQVPHV 200  
 QY 124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIM---ESANGWHD 178  
 Db 201 LSRASVGAARVAGLWGI-----LLNGHLLISTFGSGFSLSYRVTGTPSASLRWHQ 254  
 QY 179 IMFOLPEFMPGLIILFCSEKIVWSLRRRQQLARQARMKATRFIMVVAIVITCYLPSV- 237  
 Db 255 ALYLLEFPLFLLALIFAIVSIGLTRNR-GLGQAGQPARMRVLAAMVAVVITCFLPSII 313  
 QY 238 --SARLYFLWTPSSA---CDPSVHGALHITLSTYMNMLDPLVYFSSSPF 285  
 Db 314 FGMASVAFMLSACRSIDLCTQLFHG----SLAFTYILNSVLDPVLYCFSSPNF 362

RESULT 4  
 US-08-955-713-4  
 ; Sequence 4, Application US/08955713  
 ; Patent No. 5955308  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SATHE, GANESH  
 ; APPLICANT: MOONEY, JEFFREY  
 ; APPLICANT: BERGSMAN, DEBK  
 ; APPLICANT: HALSEY, WENDY  
 ; TITLE OF INVENTION: cDNA CLONE HE0AD54 THAT ENCODES A HUMAN 7-TRANS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-713-4

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Query Match 27.5%; Score 510; DB 2; Length 476;
Best Local Similarity 39.6%; Pred. No. 4e-36;
Matches 110; Conservative 47; Mismatches 101; Indels 20; Gaps 6;

QY 18 MPPLIVAFVGLGALNGVALCGFCFHMKTWKPSTVYLENLAVADFLMCLPRTDYLYR 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LAPILALEFVLGVNLSALFICHTHRTWTNTVFLVSLVADFLIISNLPURDYILL 65

QY 78 RRHAFGDI PCRVGLFTLAMNRAAGSIVFLTVVAADRYFKVVPHPHVAVTISTRVAGIVC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 HETWRFGAACKVNLFMLSTNRKASVVELTALNRYLKVKVXPHVNLNRSVGMARVVG 125

QY 138 TLWALVILGTVYLLLENHLCVQETAVSCSFPM-----ESANGWHDIMFOLEFPMIGIIL 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 GIWVILLINGKLLNTF-----SGPCLSYRVGTPKPSASLRHQALYLLFELPLALIL 180

QY 194 FCSEKIVWSLRRRQQLARQARKKATREFIMVVAIVFITCYLPSV---SARLYELWTVPS 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 FAIVSIGLTIERN-GLGQAGQORAMRVLAMVAVYTCFLFSIIIFGASWAFWLSACR 239

QY 251 A---CDPSVHGALHTLTSTYNSMLDPLVYFFSPSF 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 SLDLCTQLFHG----SLAFTYLSVLDPLVLYCFSSPNE 273

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RESULT 5
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031090
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELISHOURAGY, NABIL
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-Aug-1998

```

```

; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-130-749-2

```

```

Query Match 24.4%; Score 451.5; DB 3; Length 319;
Best Local Similarity 34.4%; Pred. No. 2.8e-31;
Matches 101; Conservative 61; Mismatches 121; Indels 11; Gaps 5;

QY 7 CRIEGTISQVMPPLIVAFVGLGALNGVALCGFCFHMKTWKPSTVYLENLAVADFLMI 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 CSAPSTVWATAVGLVGLGCLGLGNVAVALMTFLFRVVKPKYAVVYLLNALADLLAA 65

QY 67 CLPFTDYLYRRRHMAFGDIPCRVGLFTLAMNRAAGSIVFLTVVAADRYFKVVPHPHVAVT 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 CLPFLAFLVLSQAMHLGRVGCWALRFLDLSKSVGMFLAAVALDKYLRVHPRLKVN 125

QY 127 ISTRVAGIIVCTIMWALVILGTVYLLLENHLCVQETAVSCSFIMESANG----WHDIMF 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 LSPQALGVSLVLMILMVALTCPGLLISE--AAQNSTRCHSF-YSRADGFSFIWQALS 182

QY 182 QLEFFWPLGIILFCSEKIVWSLRRR-QQLARQARKKATREFIMVVAIVFITCYLPSVSAR 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 CLQFVLPFLGVFCNAGIIRALQKRLREPKQPKLQRAQALVTVVVLFCALCELPCLAR 242

QY 241 --LYELWTVPSACDPSVHGHALHTLTSTYNSMLDPLVYFFSPSPFPKFNKL 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 VLMHIFQNLGSCALCAVAHTSDVTGSLTYLHSLVLPVWYCFSSPTFRSSRRV 296

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RESULT 6
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031344
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELISHOURAGY, NABIL
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-Aug-1998
; CLASSIFICATION:

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```

Db 54 LPVAVILVFIIGLNSVAINMVFPMKPSGIVYMENLALADFLYVLTLPALIFYFN 113
QY 78 RHWAFGDI PCRVGLFTLAMNAGSIVELTVVADRYKVVPHAVNTISTRVAAGIVC 137
Db 114 KDWIFGAMCKLQRFIFHNLYGSLFUTCSAHRYSGVVYPLKSLGRLKKNNAVYISV 173
QY 138 TLWALVILGTVYLLNHLVCQET-AVSC-----ESFIMESANGWHDIMFOLEFFM 187
Db 174 LWLVIVVVGISPLFVSGTGIRKNKTIICYDTTSDBYLRSFYISM-----CTTVAMFCV 228
QY 188 PLGIILFCFVKIWSLRROQLARQARMKATRFIMVVAIVFITCYLP-----SVSAR 240
Db 229 PLVLILGCGVGLVRLAIYK-DLDNSPLRRKSYLVILVTVFAVSYIPFHVMTNLRAR 287
QY 241 LVFLMTVPSSACDPSVHGALHITLFTYMNMSMLDPLVYVFFSPSPKFNKLIKCSLKPK 300
Db 288 LDF-QTPMCAFNRVYATYQVTRGLASLNSCVDILYFLAGDTFRRLSR-----337
QY 301 QPGHKTQRPBEMPISNLGRSCISVANSFQSQSD 335
Db 338 --ATRKASRRSEANLQSKSEDMTNILSEFKONGD 370

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## RESULT 11

```

US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-707-4

```

```

Query Match 19.6%; Score 362.5; DB 3; Length 373;
Best Local Similarity 27.5%; Pred. No. 1.5e-23;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

QY 18 MPPLIIVAFVLGALNGVALCGCFHMKTKPSTVILFNLAADFLIMICLPFTDYLR 77
Db 54 LPVAVILVFIIGLNSVAINMVFPMKPSGIVYMENLALADFLYVLTLPALIFYFN 113
QY 78 RHWAFGDI PCRVGLFTLAMNAGSIVELTVVADRYKVVPHAVNTISTRVAAGIVC 137

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Db 114 KDWIFGAMCKLQRFIFHNLYGSLFUTCSAHRYSGVVYPLKSLGRLKKNNAVYISV 173
QY 138 TLWALVILGTVYLLNHLVCQET-AVSC-----ESFIMESANGWHDIMFOLEFFM 187
Db 174 LWLVIVVVGISPLFVSGTGIRKNKTIICYDTTSDBYLRSFYISM-----CTTVAMFCV 228
QY 188 PLGIILFCFVKIWSLRROQLARQARMKATRFIMVVAIVFITCYLP-----SVSAR 240
Db 229 PLVLILGCGVGLVRLAIYK-DLDNSPLRRKSYLVILVTVFAVSYIPFHVMTNLRAR 287
QY 241 LVFLMTVPSSACDPSVHGALHITLFTYMNMSMLDPLVYVFFSPSPKFNKLIKCSLKPK 300
Db 288 LDF-QTPMCAFNRVYATYQVTRGLASLNSCVDILYFLAGDTFRRLSR-----337
QY 301 QPGHKTQRPBEMPISNLGRSCISVANSFQSQSD 335
Db 338 --ATRKASRRSEANLQSKSEDMTNILSEFKONGD 370

```

## RESULT 12

```

US-09-947-922-4
; Sequence 4, Application US/09947922
; Patent No. 6680373
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,922
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-922-4

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Query Match 19.6%; Score 362.5; DB 4; Length 373;
Best Local Similarity 27.5%; Pred. No. 1.5e-23;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

QY 18 MPPLIIVAFVLGALNGVALCGCFHMKTKPSTVILFNLAADFLIMICLPFTDYLR 77
Db 54 LPVAVILVFIIGLNSVAINMVFPMKPSGIVYMENLALADFLYVLTLPALIFYFN 113

```



## RESULT 15

US-08-153-848-44  
; Sequence 44, Application US/08153848  
; Patent No. 5753804  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,848  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5759804and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 3i794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-153-848-44

Query Match 18.1%; Score 336; DB 1; Length 339;

Best Local Similarity 30.5%; Pred.No. 2.5e-21;

Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

QY	7	CRLEGDTISQVMPPELLIVAFVLGALGNVALCGFCFHMKTWKPSTVYLFNLAVADFLIMI	66
Db	23	CCQETPLENMLFASFYLLDFILAVGNLTALWLFIRDHKSGTANVFLMHLAVADLSCVL	82
QY	67	CLPFRDYLRHRHWFAGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYEKVWHPHVAVT	126
Db	83	VLPTRLVYHFGSNHMPGEIACRLTGFLYINWYASIVFLTCISADRFIAVHP---VKS	139
QY	127	ISTR--VAAGIVCT-LNALVILGVYILLENLHLCVQETAVSCSFIMESANGWHDIMFQL	183
Db	140	LKLRPLVYAHACAFLLWVAVAMAPLIVSPQVTQNTVTVCLQLYREKASHHALVSLAV	199
QY	184	EFPMPLGILLFCSPKIWSLRQRQARQPMK-KATPFTMVVAIVITCYLP-SVSARL	241
Db	200	AFTFPPTTITVTCYLLIIRSL--RQGLRVERKRLKTKAVRMIAIPLAIFLVCVPYHVRSV	257
QY	242	YFL-WTVFESSACDPSVHGAL--HITLSFTYWNMLDPLVYFSSPSPKPKYKLIKCSLK	298
Db	258	YVLHYRSHGASCATORILALANRITSCLTSLNGALDPIIMYFFVAEKFRHALCNL-LGKR	316
QY	299	PKQFGSKTORPEMPIS	316

Db 317 LKGPPSPFEGCKTNESSLS 334

Search completed: June 30, 2004, 17:24:28  
Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: June 30, 2004, 17:19:42 ; Search time 21 Seconds  
(without alignments)  
1584.870 Million cell updates/sec

Title: US-10-076-260-2

Perfect score: 1853

Sequence: 1 MYNGSCCRIEGDTISQWMP2.....ANSFQSQSDGQWDPHVEWE 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	980.5	47.5	387	2 I69202	G protein-coupled
2	364	19.6	362	2 S33733	G protein-coupled
3	362.5	19.6	373	2 JC4162	P2r receptor - bov
4	354	19.1	373	2 JC4737	G protein-coupled
5	343.5	18.5	370	2 JC5549	heptahelical P2Y5-
6	339	18.3	308	2 T05241	G protein-coupled
7	324	17.5	344	2 T09508	intron 17 purinerg
8	320	17.3	373	2 A47556	ATP receptor P2u -
9	310.5	16.8	420	2 I51667	thrombin receptor
10	309.5	16.7	363	2 I57940	somatostatin recep
11	307	16.6	391	2 C41795	somatostatin recep
12	305.5	16.5	391	2 A41795	somatostatin recep
13	305.5	16.5	391	2 A39297	somatostatin recep
14	304.5	16.4	359	2 S15450	angiotensin II rec
15	302.5	16.3	369	2 B41795	somatostatin recep
16	302	16.3	364	2 JQ1488	somatostatin recep
17	302	16.3	399	2 I48705	bradykinin B2 rece
18	300.5	16.2	369	2 A45291	proteinase activat
19	300.5	16.2	369	2 D41795	somatostatin recep
20	300	16.2	328	2 I55450	G protein-coupled
21	300	16.2	384	2 A47449	brain-specific som
22	300	16.2	428	2 A44021	somatostatin recep
23	299.5	16.2	369	2 JC2083	somatostatin recep
24	299	16.1	388	2 JN0695	somatostatin recep
25	298.5	16.1	418	2 A46226	somatostatin recep
26	298.5	16.1	432	2 A43448	thrombin receptor
27	298	16.1	428	2 S10508	probable G protein
28	297	16.0	397	2 S66518	proteinase-activat
29	296.5	16.0	346	2 S29248	somatostatin recep

30 296 16.0 359 2 A48857 angiotensin II rec  
31 296 16.0 375 2 A54946 P-2U nucleotide re  
32 295 15.9 384 2 JC4629 somatostatin recep  
33 294 15.9 372 2 J38532 delta opioid recep  
34 292.5 15.8 361 2 JC5653 G protein-coupled  
35 292 15.8 371 2 JC5498 G protein-coupled  
36 291.5 15.7 359 2 S44425 angiotensin II rec  
37 291.5 15.7 359 2 JC2134 angiotensin II rec  
38 290 15.7 372 2 S34592 delta opioid recep  
39 289 15.6 359 2 JC1104 angiotensin II rec  
40 288 15.5 355 2 A45177 chemokine (C-C) re  
41 288 15.5 372 2 B48227 delta opioid recep  
42 287.5 15.5 365 2 S68208 G protein-coupled  
43 287.5 15.5 371 2 JC5796 probable chemoatrac  
44 286.5 15.5 359 2 JH0621 angiotensin II rec  
45 286.5 15.5 423 2 JC7677 allatostatin recep

## ALIGNMENTS

## RESULT 1

I69202

G protein-coupled receptor HM74 - human

C:Species: Homo sapiens (man)

C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 19-May-2000

C:Accession: I69202

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte che

A:Reference number: I54751; MUID:94092629; PMID:7505609

A:Accession: I69202

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867

C:Genetics:

A:Gene: HM74

C:Superfamily: G protein-coupled receptor 4

Query Match 47.5%; Score 880.5; DB 2; Length 387;  
Best Local Similarity 52.2%; Pred. No. 5.4e-74;  
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCRIEIGDTISQWMPILLIVAFVLGALGNVALGFCFPHMKTKPSTVYLFNLAVADFL 64  
Db 17 NCCVFRDDFIKVLPPVLGLEIFGLLGNGLAWIFCFHLKSKSSRIPLFNLAVALFL 76  
QY 65 MICLPFRDYYLRRRHAFGDIPCRVGLFTLAMNRAGSIVELTVVAAADRYKVVHPHAAV 124  
Db 77 IICLPFVMDYYVRSNDNFQDIPCELVLFPMAMNRQSSIIELTVVAVDRYFVVPHHAL 136  
QY 125 NTISTRVAAGIVCTVWALVILGTVYLLLENHLCVQSTAVSCSFIMESANGWHIMFOLB 184  
Db 137 NKISNMTAAIISCLLWGITVGLTVHLLKLLIQNGPANVCISFISCHTFRWHEAMFLLE 196  
QY 185 FFWPLGILICSFIVMSLRROQLARQAKKATRTMTVAIVITCYLPSVSAELYEL 244  
Db 197 FLPLGILILFCSARIITWSLRQR-QMDRHAKTKRAITFMVVAIVFVIFCLFSPVVRIRIF 255  
QY 245 WTVPSA---CD--PSVHGALHITLSFTYNNMLDPLVYFSSPSFPKFKYKLCIKSLKP 299  
Db 256 WLLHTSTQNCVRSVVDLAFITLSFTYNNMLDPLVYFSSPSFPNFFSLINRCLOR 315  
QY 300 KQPGHSHKTQPERPMPLNGLRRSCISVANFSQSQSDQWDNP 340  
Db 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPMSP 355

## RESULT 2

S33733

G protein-coupled receptor - chicken

C:Species: Gallus gallus (chicken)



C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-Sep-1999  
C/Accession: S33733  
R/Species: Bos primigenius taurus (cattle)  
R/Author: T.E.; Simon, J.; Kriehke, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock  
R/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.  
A/Reference number: S33733; MUID:93285340; PMID:8508924  
A/Accession: S33733  
A/Status: Preliminary  
A/Molecule type: mRNA  
A/Residues: 1-362 <WEB>  
A/Cross-references: EMBL:X73268; NID:g935084; PIDN:CAA51716.1; PID:g935085  
C/Superfamily: ATP receptor P2u  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.6%; Score 364; DB 2; Length 362;  
Best Local Similarity 29.1%; Pred. No. 4.7e-26;  
Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPPLIVAFVLGALNGVALGFCFHMKTWKESTVYVLENLAVADFLMLICLFRDTDYLR 77  
DB 43 LPTVYLFIIGFLGNSVAIMFVPHMPWGSIGSYMFNLADFLYVLTLPALIFYFN 102  
QY 78 RHMAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHVAVNTISTRVAAGIVC 137  
DB 103 KTDWIFGDVCMCKLQRFIFHNLYGSLFILTCSVHRVYGVVHPLKSLGRLKKKNVYVSS 162  
QY 138 TLMAVLIL-----GTVLLLENHLCVQETA-----VSCSFIMESANGWHD 178  
DB 163 LVMALWVAIVAPILFYSGTGVRRNKTIITCYDTADEYLSRVYGMCTVFN----- 214  
QY 179 IMFQLEFMPGILIFCSFKIWSLRRRQQLARQARKKATRFIMVAIVFITCYLP--- 235  
DB 215 -----FCIPFVLICGCVGLIVKALYK-DLDNSPLRKSIVLVIIVTVFAVSILPHV 267  
QY 236 ----SVSARLYFLMTVPSSACDPSVHGALHITLSTFYNNMSLDPVLYFFSPSPFKFYNK 291  
DB 268 MKTLNLRARLDF-QPEQCAFNKDYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR 326  
QY 292 LXICSLKPKQGHKTKQRPPEMPISNL 318  
DB 327 ATRKSRSEEP--NVQSKSEMTNLIL 351

RESULT 3  
JC4162  
P2Y receptor - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 12-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 24-Sep-1999  
C/Accession: JC4162  
R/Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.  
Biochem. Biophys. Res. Commun. 212, 648-656, 1995  
A/Title: Cloning and characterization of a bovine P2Y receptor.  
A/Reference number: JC4162; MUID:95352058; PMID:7626079  
A/Accession: JC4162  
A/Molecule type: mRNA  
A/Residues: 1-373 <HEN>  
A/Cross-references: EMBL:X87628; NID:q1032484; PIDN:CAA60958.1; PID:g1032485  
A/Experimental source: aortic endothelial cell  
C/Genetics:  
A/Gene: bomp2Y  
C/Superfamily: ATP receptor P2u  
C/Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:52-77/Domain: transmembrane #status predicted <TM1>  
F:88-111/Domain: transmembrane #status predicted <TM2>  
F:124-150/Domain: transmembrane #status predicted <TM3>  
F:171-191/Domain: transmembrane #status predicted <TM4>  
F:214-237/Domain: transmembrane #status predicted <TM5>  
F:261-282/Domain: transmembrane #status predicted <TM6>  
F:305-328/Domain: transmembrane #status predicted <TM7>  
F:11, 27, 113, 197/Binding site: carbonylate (Asn) (covalent) #status predicted  
F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.6%; Score 362.5; DB 2; Length 373;

Best Local Similarity 27.5%; Pred. No. 6.7e-26;  
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

QY 18 MPPLIVAFVLGALNGVALGFCFHMKTWKESTVYVLENLAVADFLMLICLFRDTDYLR 77  
DB 54 LPAVVILFIIGFLGNSVAIMFVPHMPWGSIGSYMFNLADFLYVLTLPALIFYFN 113  
QY 78 RHMAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHVAVNTISTRVAAGIVC 137  
DB 114 KTDWIFGDVCMCKLQRFIFHNLYGSLFILTCSVHRVYGVVHPLKSLGRLKKKNVYVSS 173  
QY 138 TLMAVLILGTVYVLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEPFX 187  
DB 174 LVMALWVVGISPIIFYSGTGVRRNKTIITCYDTSDYLSRYFIYSM-----CTTVAMFCV 228  
QY 188 FLGIILFCSEKIVWSLRRRQQLARQARKKATRFIMVAIVFITCYLP-----SVSAR 240  
DB 229 FLVLLICGCVGLIVKALYK-DLDNSPLRKSIVLVIIVTVFAVSIFPHVVKTNLRAR 287  
QY 241 LYFLMTVPSSACDPSVHGALHITLSTFYNNMSLDPVLYFFSPSPFKFYNKIKCSLKEK 300  
DB 288 LDF-QTPENCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR----- 337  
QY 301 OPGHSHKTPRPEMPISNLGRRSICISVANSFQSQSD 335  
DB 338 --ATRKSRSEANTQSKSEMTNLILSEFKQNGD 370

RESULT 4  
JC4737  
G protein-coupled receptor P2Y1 - human  
N/Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor  
C/Species: Homo sapiens (man)  
C/Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 17-Nov-2000  
C/Accession: JC4737; JC4615; S54253  
R/Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.  
Biochem. Biophys. Res. Commun. 221, 588-593, 1996  
A/Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.  
A/Reference number: JC4615; MUID:96158962; PMID:8579591  
A/Accession: JC4615  
A/Molecule type: mRNA  
A/Residues: 1-373 <AVY>  
A/Cross-references: GB:S81950; NID:q1839438; PIDN:AA847091.1; PID:g1839439  
R/Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.  
Biochem. Biophys. Res. Commun. 218, 783-788, 1996  
A/Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.  
A/Reference number: JC4615; MUID:96158962; PMID:8579591  
A/Accession: JC4615  
A/Molecule type: mRNA  
A/Residues: 1-373 <AVY>  
A/Cross-references: GB:U42029; NID:q1147730; PIDN:AAA97872.1; PID:g1147731  
A/Experimental source: erythro leukemia cells  
R/Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.  
submitted to the EMBL Data Library, May 1995  
A/Description: Cloning of a human putative P2Y receptor.  
A/Reference number: S54253  
A/Accession: S54253  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-137,139-373 <LEO>  
A/Cross-references: EMBL:Z49205; NID:g979835; PIDN:CAA89066.1; PID:g979836  
C/Comment: This receptor belongs to a family of G protein-coupled receptors. It respon  
C/Genetics:  
A/Gene: P2Y1; GDB:P2RY1  
A/Cross-references: GDB:677125; OMIM:601167  
A/Map position: 3pter-3qter  
C/Superfamily: ATP receptor P2u  
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pr  
F:52-77/Domain: transmembrane #status predicted <TM1>  
F:88-111/Domain: transmembrane #status predicted <TM2>  
F:124-152/Domain: transmembrane #status predicted <TM3>  
F:171-191/Domain: transmembrane #status predicted <TM4>  
F:214-237/Domain: transmembrane #status predicted <TM5>

F\_261-282/Domain: transmembrane #status predicted <TM6>  
F\_305-328/Domain: transmembrane #status predicted <TM7>  
F\_11, 27, 113, 197/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F\_258, 336/Binding site: phosphate {Ser} (covalent) (by protein kinase A) #status predicted  
F\_330, 339/Binding site: phosphate {Thr} (covalent) (by protein kinase C) #status predicted  
F\_343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen

Query Match.	19.1%;	Score 354;	DB 2;	Length 373;	
Best Local Similarity	29.2%;	Pred. No. 4.2e-25;			
Matches 93;	Conservative	66;	Mismatches 132;	Indels 28;	Gaps 8;
Qy	18	MPPELLIVAFVLGALNGVALCGCFERHMKWKPKSTWYLFNLAVADFLMCLCUPRTDYVLR	77		
Db	54	LPVAIVLFIIGELGNSVALWMPFHHKPKSGSIVYMFNLALADFLVLTLPALIFITFN	113		
Qy	78	RRHWAFGDIPICVGLGFTLMMNRAGSIVFLTVVAADRYFKVHPHPHAVNTISTRVAAGTVC	137		
Db	114	KTDWIFGDGMCKLGRFIFHYNLYGSIILFTCSAHRYSGVVYPLKSLGRLLKKNKAICISV	173		
Qy	138	TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLSPFK	187		
Db	174	LVMLIVVVAISPILFYSGTGVGRKNKTIICYDTSDEVLSRYFISM-----CTTVAMFCV	228		
Qy	188	PLGLILFCSEKIVMSLRERQQLARQAKMKCATRIMVVAIVFICYLP-----SVSR	240		
Db	229	PLVILGCGYGLIVTALYIK-DLDSNPTRRKSIYIIVLTVFAVSYIFPHVWKTNNLR	287		
Qy	241	LYFLWTVPSACDSPVHGALHITLSFTYNNMLDPLVYFESSFPFKYNNKLKICSUKPK	300		
Db	288	LDF-QTPAMCAFNDRVVATYQVTRGLASLNSCVDPILYFLAGDTFRR--RLSRATRKA	343		
Qy	301	QPGHSKTQ-RPEEMPINL	318		
Db	344	RRSEANLQSKSEDMTNIL	362		

```

RESULT 5
JC5549
heptahelical P2Y5-like receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C:Accession: JC5549
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A:Reference number: JC5549; MUID:97366605; PMID:9223435
A:Accession: JC5549
A:Molecule type: DNA
A:Residues: 1-370 <JAN>
A:Cross-references: DDBJ:AF005419; NID:G2240034; PIDN:AAB66322.1; PID:G22400035
C:Superfamily: ATP receptor P2u

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Query Match.	18.5%	Score 343.5	DB 2	Length 370
Best Local Similarity	31.0%	Pred. No. 3.9e-24		
Matches 94	Conservative 52	Mismatches 130	Indels 27	Gaps 10
Qy	24	VAFVLGALGVGVALCGCFEHKTKWKPSTVYLFNLAVADELLMICLPFTDLYLRRRWAF	83	
Db	48	VVFILGILITSVSLFVFCFRKMRSETAFTNLAVSGLLFVCTVLPFKL-FYNENRHWP	106	
Qy	84	GDIPCRVFLTLANVRAGSIIVFLTVAADRYFKVYHPHHAVNTISTRVAGIVCT-LWAL	142	
Db	107	GDITLCKISGTAFNLINYGSMFLFCISVDRELAIVYPPRS-RTIRTRNSAIVCAGWIL	165	
Qy	143	VILGTVYLLLENHLICVQETAVSCSFESANGMHIDIMFOLE-----PFMPLGILF	195	
Db	166	VLSGGISASLFTSTNNVNAITTC--PEGLSKRVKTV-SKITIFIEVVGFIIPLINVSC	223	
Qy	196	SFKIVSLRRQOLAR-QARNKKATRIMVAIVFICTYLPSPSARLYPLTWESSAC--	252	
Db	224	SSVVLRTLRKPATUQIGTNKKKVLKMTVHMAVFWVCFFPYN--VLELYALVRSOAIT	281	
Qy	253	----DPSVHGALHITLSTFYNNSMDELIVYFESSFPFK-FYNKIKTCSLKPQGHSKT	307	

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Db      282  NCFLERFKIMYPILCLATLNCDFPIYYFTLESFQSFYINAH1-----RMESLFTK 336
      :      |||      :|||      :|||      :|||      :|||      :|||
QY      308  QRP 310
      :      :      :
Db      337  ETP 339

RESULT 6
I50241
G protein-coupled receptor 6H1 - chicken
N:Alternate names: purinoceptor 6H1
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
C/Accession: I50241; JG4618
R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A/Title: Identification of a G protein coupled receptor induced in activated T
A/Reference number: I50241; PMID:93329058; PMID:8939036

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## RESULT 6

G protein-coupled receptor 6H1 - chicken  
 N:Alternate names: purinoceptor 6H1  
 C:Species: Gallus gallus (chicken)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 02-Jun-2000  
 C:Accession: I50241; JC4618  
 R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
 J. Immunol. 151, 628-636, 1993  
 A:Title: Identification of a G protein coupled receptor induced in activated T cells.  
 A:Reference number: I50241; MUID:93329058; PMID:8393036  
 A:Accession: I50241  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <XAP>  
 A:Cross-references: GB:I506109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 R:Webb, T.B.; Kaplan, M.G.; Barnard, E.A.  
 Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
 A:Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
 A:Reference number: JC4618; MUID:96190677; PMID:8619790  
 A:Accession: JC4618  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <WEB>  
 A:Cross-references: GB:I506109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 A:Experimental source: T-cells  
 C:Comment: This receptor plays a role in T-cell activation.

Query Match	18.3%;	Score 339;	DB 2;	Length 308;
Best Local Similarity	30.3%;	Pred. No. 8.3e-24;		
Matches	91;	Conservative	56;	Mismatches 123;
		Indels	30;	Gaps 10;

Qy	24	VAFVLGALGNVALCGCFHHKTKWKPSTWYLFNLNLAVALDFLWICLPFRDYYLRRRHAF	83
Db	23	MVFVLGLIANGVAIYFTFLKVRNETTTVMNLNLAISDLLEFVFTLPERI-YFVYVRNMPF	81
Qy	84	GDIPCRVGLFTLANRAGSTVFLFWAADRYKVVHPHNAVNTISTRVAAGIVC-TLWAL	142
Db	82	GDVICKLSVILFYNTMTGSLIFLTCISVDRLAIWHPPRS-KTLRTKKNRAIVCVAVIT	140
Qy	143	VILGTW---YLLLENHLICVOETAVSCSFIMESANGMHDIMPQL-----EENPLGII	192
Db	141	VLAGSTPASPFQSTNRNQNETQRTCFENF---PESTWTKYLSRIVFTIEVGFIFPLIN	197
Qy	193	LFQSEKIWSLRRQQOLAR-QARKMKATRFIMVAIVFITCYLP-SVSARLYELW---TV	247
Db	198	VTGSTVHRTLNKPLTLISRNKLSKKKVLKMLFVHLVIFCFCFVYNITLILYSLRMTQTW	257
Qy	248	PSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPFKYNKLIKCSLKPQGHSKT	307
Db	258	INCSVVTAVTMYPTVLTICIAVSNCCFPYVYFSTDTNSE-----LDKCOOQHONT	308

RESULT 7  
T09508

intron 17 purinergic receptor P2Y5 - human  
N:Alternate names: G-protein coupled receptor  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
R:Accession: T09508  
R:Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.  
submitted to the EMBL Data Library, April 1997  
A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene.  
A:Reference number: Z16705  
A:Accession: T09508  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-344 <BOR>  
A:Cross-references: EMBL:AF000546; NID:G2232068; PID:G2232069  
C:Genetics:  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.5%; Score 324; DB 2; Length 344;  
Best Local Similarity 30.1%; Pred. No. 2.3e-22;  
Matches 98; Conservative 44; Mismatches 150; Indels 34; Gaps 8;

QY 24 VAFVGLGNGVAGVCGFCHMKTKWPKSTVYLFNLAVADFLIMICLPFRDYYLRRHWAF 83  
DB 26 MVFVGLVSNCAIYIFICLVKRNETHYMINLAMSLLFVFLPFRI-EYFTTRNWP 84  
QY 84 GDIPCRVGLFTLAMRAGSIVFLTVAAADRYKVVHPHVAHTISTRVAAIGVCT-LWAL 142  
DB 85 GDLCKLSVMLFYTNMYSILFLTCISVDRLAIVYFYS-KTLRTKRNKIVCTGVWLT 143  
QY 143 VILGT--VYLLLENHLCVQETAVSCSFIMESANGHMDIMQL-----EFFMPLGLIL 193  
DB 144 VIGGSAPAVFVQSTHSGQNNASEACFENFEAT--WKYLSRIVFIFIVGFFIPLILNV 201  
QY 194 FCSFKIVSLRRQQLARQARK-KATRFIMVAIVFTICVLP-SVSARLYFL---WTVP 248  
DB 202 TCSSMWLKLKYPVLSKSKNKYKVKMIFVHLIIFCFCFVYNNILLYSLVLTQTFV 261  
QY 249 SSACDPSYHGALHITLSTYNNMMLDPLVYFSPSPFKFYNKIKI 294  
DB 262 NCSVVAARVTVPIFLCIAVSNCCFDPIVYFSDT---IQNSIKM 304

RESULT 8  
A47556  
ATP receptor P2u - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
R:Accession: A47556  
R:Rustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993  
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.  
A:Reference number: A47556; MUID:93281707; PMID:7685114  
A:Accession: A47556  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-373 <LUS>  
A:Cross-references: GB:114751; NID:G309457; PID:AAA39871.1; PID:G309458  
C:Superfamily: ATP receptor P2u  
C:Keywords: transmembrane protein

Query Match 17.3%; Score 320; DB 2; Length 373;  
Best Local Similarity 30.1%; Pred. No. 6e-22;  
Matches 98; Conservative 44; Mismatches 150; Indels 34; Gaps 8;

QY 4 GSCCRTEGTISQVMPPLIVAPVLGALNGVAGVCGFCHMKTKWPKSTVYLFNLAVADFL 63  
DB 22 GYKCRNEDPKVILLPVSVGVVGLGLNVLVYLFCLKLTWASTYMFHLVSDSL 81  
QY 64 LMICLPFRDYYLRRSHWAFGDIPCRVLFTLAMRAGSIVFTTVAAADRYKVVHPHHA 123  
DB 82 YAALELLVYVYARGDHWPFSTVLCKLVRFVFLYTNLYCSILFLTCISVHRCGLVLRPLHS 141

QY 124 VNTISTRVAAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESAN 174  
DB 142 LRNGRARIARVAANVWVLAQAPVLYFTTISVGRITRCHDTSARELFSHEVAYSS- 200  
QY 175 GMDHIMFQLEFFMPLGILFCSFKIVSLRRQ-----LAROARKKATRFIMVA 226  
DB 201 ----VMLGLFVAFVSVILVC--VYLMARLLKPAYTGTGGPRKR--KSVRTIALVL 251  
QY 227 IVITCTVLP-SVSARLYFLMTVPSSACDP--SVHGALHITLSTYNNMMLDPLVYFSSP 283  
DB 252 AVFALCFLPFHVTITLYSERSLDSCHTNAINNAYKITRPLASANSCLDPVLYFLAQ 311  
QY 284 SFPKFNKLIKCSLKPQPGHSTQK 309  
DB 312 RLVRFARDAK-----PPTPTSPQAR 333

RESULT 9  
151667  
Thrombin receptor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
R:Accession: 151667  
R:Gerzsten, R.B.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.;  
Nature 368, 648-651, 1994  
A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extracellular domain.  
A:Reference number: 151667; MUID:94195429; PMID:8145852  
A:Accession: 151667  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-420 <GER>  
A:Cross-references: EMBL:U09632; NID:G495197; PIDN:AAA18498.1; PID:G495198

Query Match 16.8%; Score 310.5; DB 2; Length 420;  
Best Local Similarity 28.0%; Pred. No. 5.2e-21;  
Matches 88; Conservative 56; Mismatches 133; Indels 37; Gaps 10;

QY 14 ISQVMPPLIVAFVGLGALNGVAGVCGFCHMKTKWPKSTVYLFNLAVADFLMCLPFRD 73  
DB 100 LTKFVPSLYTVFVIGVGLPLNLLAIIFLFKMKVRKPAVVYMLNLAIDAVFVSVLPFKIA 159  
QY 74 YVLRHRHWAIPDIPCRVGLFTLAMRAGSIVFLTVAAADRYKVVHPHVAHTISTRVAA 133  
DB 160 YHLSGNDMLFGFGMCRIVTAIFYCNMYSVLIASISVDRLAVVYFVHSLSW-RTMSRA 218  
QY 134 GIVCT-LWALVILGTVYLL--ENHLCVQETAVSCSFIMESANGHMDIMQ---LEF 185  
DB 219 YMACSFIMLISASTIPLLVTSQTKIPRLDITTCVLDLKDLDKDFIYVYFSSFCILPF 278  
QY 186 FMPLGILFCSFKIVSLRRQQLARQARKKATRFIMVAIVFTIC-----YL 234  
DB 279 FVFFITTCYIGIRSL--SSSIENSCCKTRALFLAVVLCVFIICFGPTNVLFLTHYL 337  
QY 235 PSVSARLYFLMTVPSSACDPSPVHGALHITLSTYNNMMLDPLVYFSSSPFKFYNKIKI 294  
DB 338 QEANEFLYPAYIL--SACVGSV-----SCCLDPLIYVYASQCCRYLSL-L 381

QY 295 CSLKPKQPGHSTQK 308  
DB 382 CCRKVSSEPGSSTGQ 395

RESULT 10  
157940  
somatostatin receptor 5 - rat  
N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 24-Nov-1999  
C:Accession: 157940; S39244  
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.  
Mol. Pharmacol. 42, 939-946, 1992  
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pr

C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

A;Reference number: I57940; MUID:93125499; PMID:1362243

A;Accession: I57940

A;Status: preliminary; translated from GB/EMBL/DDJ

A;Molecule type: mRNA

A;Residues: 1-363 <OCAL>

A;Cross-references: GB:I04535; NID:9409238; PIDN:AAAI7029.1; PID:g409239

R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 1278, 1993

A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57949; MUID:94088493; PMID:8264565

A;Accession: I57949

A;Status: preliminary; translated from GB/EMBL/DDJ

A;Molecule type: mRNA

A;Residues: 341-363 <OCA2>

A;Cross-references: GB:967370; NID:g455947; PIDN:AAB29371.1; PID:g455948

R;Penetta, R.; Greenwood, M.; Patel, Y.C.

submitted to the EMBL Data Library, August 1993

A;Description: Correction of the nucleotide and amino acid sequence of the rat somatosta

A;Reference number: S39244

A;Accession: S39244

A;Molecule type: mRNA

A;Residues: 329-363 <PEN>

A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAAS2825.1; PID:g433912

C;Genetics:

A;Gene: SSTR5

C;Superfamily: vertebrate rhodopsin

Query Match 16.7%; Score 309.5; DB 2; Length 363;  
Best Local Similarity 29.6%; Pred. No. 5.5e-21;  
Matches 96; Conservative 53; Mismatches 146; Indels 27; Gaps 9;

QY 17 VMPELLIVAFVGLGNGVLCGFCFHMKTWKPSTVYFLNLAADVADFLMCLPFRDYYL 76  
DB 39 LPEVLIVCTVLSGNLIVVYVLRHAKMTVTNYLLNLAADVADFLMCLPFRDYYL 98  
QY 77 RRRHWAFGDIPCRVGLFTLMMNRAGSIVFLTVADRYFKVHPHVAHVNTISTRVAAGIV 136  
DB 99 VVSYWPGSFLCLVLTLDGNGQTSIFCLMWSVDYLVAVHPLRSARWRPRVAKMAS 158  
QY 137 CYLWALVILGTVYLLNHLCTQETAVSCSFIMESANGMHDIMFO----LFFFPPLGII 192  
DB 159 RAAYVFLMSLPLAV--FADVQEGMTCNLSPVGLWGAFFITYTSLVGLFGPLVI 216  
QY 193 LFCSEKIVWSLR---RQQLARQARK-KATRFIMVAIVFICPYLPSVSARLYFL-WTV 247  
DB 217 CLCYLLIVVYKVAAGNKGVSRRSEKPKVTRMVMVVLVFGCLPFFFTVIVNLAFTL 276  
QY 248 PSSACDPSVGHGALHITLSFTYMNMSLDPLVYFSSPSPFKYKLIKIC-----SLKP 299  
DB 277 PE---EPTSNGLYFFVVLVSYANSCANPLYGLSDNFRSFRKV-LCLRGGYGMEDADA 332  
QY 300 KQCHSKTORPEMPISNLRGSC 323  
DB 333 IEPRDKSGRPQ----ATLPTSC 352

## RESULT 11

C41795

somatostatin receptor 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 31-Dec-1993 #text\_change 24-Nov-1999

C;Accession: C41795

R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A;Title: Cloning and functional characterization of a family of human and mouse somatost

A;Reference number: A41795; MUID:92108031; PMID:1346068

A;Accession: C41795

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-391 <YAM>

A;Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059

C;Superfamily: vertebrate rhodopsin

Query Match 16.6%; Score 307; DB 2; Length 391;

Best Local Similarity 25.7%; Pred. No. 1e-20;

Matches 85; Conservative 62; Mismatches 130; Indels 54; Gaps 9;

QY 4 GSCCRIEGD-----TISQMPPLLIIVAFV-----LGALNGVLCGFCF 40  
DB 24 GACSRGPGSAAAGMBEPGRNASQMTLSEGGSAIILSFIYSVCLVGLCGNSKVIYVI 83  
QY 41 CFEMKTWKPSTVYFLNLAADVADFLMCLPFRDYYLRRHWAFGDIPCRVGLFTLMMNR 100  
DB 84 LRYAKMTATNYIYLNLAIADLMLSLVPFLVSTL-LRHWPFGLLCRLVSLVDVAVNM 142  
QY 102 GSIIVFLTVADRYFKVHPHVAHVNTISTRVAAGIVCTLWALVILGTVYLLNHLVCV-Q 159  
DB 143 TSIYCLIVLSVDYRYAVVHPVPIKAAARYRPTVAKVNLGVNLVSLVILVIFVFSRTA 202  
QY 160 ETAVSCSFIMESANGMHD----IMFQLEFPKPIGLIILFC-----SEKIVWSLR 204  
DB 203 DGTVACNMLPEPAQRMLVGVFLYITFLMGFLPLVGAICLCYVLIILAKRMVALKAGWQ 262  
QY 205 RQQLARQARK-KATRFIMVAIVFICPYLPSVSARLYFLTVPSACDPSVGHGALHITL 264  
DB 263 KRSE-----RKITLVMVMVMVNVFICWPPFYVQLVNVVFAEQDDAT-----VSQ 309  
QY 265 SFTYMNMSLDPLVYFSSPSPFKYKLIKIC 295  
DB 310 ILGYANSCANPLYGLSDNFRSFRKI-LC 339

## RESULT 12

A41795

somatostatin receptor 1 - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 24-Nov-1999

R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A;Title: Cloning and functional characterization of a family of human and mouse somat

A;Reference number: A41795; MUID:92108031; PMID:1346068

A;Accession: A41795

A;Molecule type: DNA

A;Residues: 1-391 <YAM>

A;Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434

A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBI:P:74768)

C;Genetics:

A;Gene: GDB:SSTR1

A;Cross-references: GDB:134185; OMIM:182451

A;Map position: 14q13-14q13

A;Introns: #status absent

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; ph

F;58-84/Domain: transmembrane #status predicted <TM1>

F;95-120/Domain: transmembrane #status predicted <TM2>

F;132-153/Domain: transmembrane #status predicted <TM3>

F;173-195/Domain: transmembrane #status predicted <TM4>

F;220-250/Domain: transmembrane #status predicted <TM5>

F;269-296/Domain: transmembrane #status predicted <TM6>

F;302-326/Domain: transmembrane #status predicted <TM7>

F;444,48,381/Binding site: carboxylate (Asn) (covalent) #status predicted

F;130-208/Disulfide bonds: #status predicted

F;172/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predi

F;265/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predi

F;339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.5%; Score 305.5; DB 2; Length 391;

Best Local Similarity 26.3%; Pred. No. 1.4e-20;

Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;

QY 10 EGDITISQVMPPLLIIVAFV-----LGALNGVLCGFCFHMKTWKPSTVYFLNLAAD 63  
DB 47 QNGTLSEGGSAIILSFIYSVCLVGLCGNSKVIYILRYAKMTATNYIYLNLAIADSL 106



Search completed: June 30, 2004, 17:23:53  
Job time : 23 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2004, 03:49:46 ; Search time 4415 Seconds  
(without alignments)  
10190.276 Million cell updates/sec

Title: US-10-076-260-1

Perfect score: 1038

Sequence: 1 atgtacacgggtcgtcgtg.....ccacattgttgagtggtgac 1038

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb\_hgt:\*  
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4: gb\_om:\*  
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7: gb\_ph:\*  
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30: em\_hgt\_hum:\*  
31: em\_hgt\_inv:\*  
32: em\_hgt\_other:\*  
33: em\_hgt\_mus:\*  
34: em\_hgt\_pln:\*  
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36: em\_hgt\_mam:\*  
37: em\_hgt\_vrt:\*  
38: em\_sy:\*  
39: em\_hgt\_hum:\*  
40: em\_hgt\_mus:\*  
41: em\_hgtg\_other:

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1038	100.0	1038	6	AX592617	AX592617 Sequence
2	1038	100.0	1038	6	BD140826	BD140826 Novel G P
3	1038	100.0	1041	6	AX147834	AX147834 Sequence
4	1038	100.0	1041	6	AX148182	AX148182 Sequence
5	1038	100.0	1041	6	AX299705	AX299705 Sequence
6	1038	100.0	1041	6	AX375434	AX375434 Sequence
7	1038	100.0	1041	6	AX521883	AX521883 Sequence
8	1038	100.0	1041	6	AX675169	AX675169 Sequence
9	1038	100.0	1041	6	BD144279	BD144279 Novel G-P
10	1038	100.0	1041	9	AB083631	AB083631 Homo sapi
11	1038	100.0	1041	9	AF411110	AF411110 Homo sapi
12	1038	100.0	1050	6	AX338373	AX338373 Sequence
13	1038	100.0	1083	6	AX305131	AX305131 Sequence
14	1038	100.0	1083	6	AX549382	AX549382 Sequence
15	1038	100.0	1372	6	AX305131	AX305131 Sequence
16	1038	100.0	1441	9	AB065866	AB065866 Homo sapi
17	1038	100.0	1730	6	AX277635	AX277635 Sequence
18	1038	100.0	2331	6	AX299707	AX299707 Sequence
19	1038	100.0	2345	9	AF385432	AF385432 Homo sapi
20	1038	100.0	3612	9	AF385431	AF385431 Homo sapi
21	1038	100.0	204793	9	AC026333	AC026333 Homo sapi
22	1036.4	99.8	1041	6	AX395171	AX395171 Sequence
23	1036.4	99.8	1194	6	AX395169	AX395169 Sequence
24	1036.4	99.8	2748	9	AK122859	AK122859 Homo sapi
25	1034.8	99.7	1104	6	AX338374	AX338374 Sequence
26	888	85.5	888	6	AX147766	AX147766 Sequence
27	888	85.5	888	6	AX521815	AX521815 Sequence
28	724.4	69.8	1668	6	AX592621	AX592621 Sequence
29	722.8	69.6	3251	6	AX592619	AX592619 Sequence
30	722.8	69.6	256368	2	AC122753	AC122753 Mus muscu
31	721.2	69.5	238844	2	AC097683	AC097683 Rattus no
32	578.4	55.7	185956	2	AC129582	AC129582 Mus muscu
33	402.8	38.8	1254	6	AX704524	AX704524 Sequence
34	372.4	35.9	1174	6	AX384661	AX384661 Sequence
35	372.4	35.9	1295	9	AY148884	AY148884 Homo sapi
36	372.4	35.9	1361	6	BD133032	BD133032 HM74 rece
37	369.2	35.6	1092	6	AX148194	AX148194 Sequence
38	369.2	35.6	1492	6	AB083632	AB083632 Homo sapi
39	369.2	35.6	1492	9	AB065876	AB065876 Sequence
40	369.2	35.6	2065	9	BC063461	BC063461 Homo sapi
41	367.6	35.4	1092	6	AX704522	AX704522 Sequence
42	367.6	35.4	1164	6	AR308634	AR308634 Sequence
43	367.6	35.4	1564	9	AB065865	AB065865 Homo sapi
44	367.6	35.4	2049	9	BC038955	BC038955 Homo sapi
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# ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX592617  
Sequence 1 from Patent WO2003736.  
AX592617  
AX592617.1 GI:28144739

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Elliot, S.G., Rogers, N. and Busse, L.A.  
G-protein coupled receptor molecules and uses thereof  
Patent: WO 02083736-A 1 24-OCT-2002;

Pred. No. is the number of results predicted by chance to have a

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Amgen, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="unnamed protein product"
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TRFTMVAVIPIITCLPSVSLARLVFLWTPSSACDPSVHGALHILFTSNMIDPL
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Query Match      100.0%; Score 1038; DB 6; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTACAAACGGTCTGCTCGGATCGAGCGGAGACACCATCTCCAGGTGATCCCGCG 60
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DB 181 GATTTCTCTCTATGATGCTGCTGCTTTTGGACAGACATATTACTCAGACGTAGACAC 240
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DB 241 TGGGCTTTTGGGACATTCCTTCCGAGTGGGCTCTTCCAGTGGCCATGACAGCGGC 300
QY 301 GGGAGCATGCTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAAGTGTCCACCCC 360
DB 301 GGGAGCATGCTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAAGTGTCCACCCC 360
QY 361 CACCAACGGTGAACACTATCTCCACCGGCTGGGCTGGGCTGGCATCTGACCCCTGTGG 420
DB 361 CACCAACGGTGAACACTATCTCCACCGGCTGGGCTGGGCTGGCATCTGACCCCTGTGG 420
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DB 421 GCGCTGGTCACTCTGGGAACAGTGTATCTTTTGGTGGAGAACCACTCTGCGTGGCAAG 480
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DB 1021 CACATTTGATGAGTGGCAC 1038

RESULT 2
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LOCUS
DEFINITION
BD140826
VERSION
BD140826.1 GI:23235771
KEYWORDS
WO 0202767-A/1.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1038)
AUTHORS
Shibata,S., Horikoshi,K., Taniyama,Y., Shintani,Y. and Miyajima,N.
TITLES
Novel G protein-coupled receptor protein and its DNA
JOURNAL
TAKEDA CHEMICAL INDUSTRIES LTD.SACHIO SHIBATA,KENICHI HORIKOSHI,
YOSHIO TANIYAMA,YASUSHI SHINTANI,NOBUYUKI MIYAJIMA
COMMENT
OS Homo sapiens (human)
PN WO 0202767-A/1
PD 10-JAN-2002
PF 02-JUL-2001 WO 2001JP005711
PR 04-JUL-2000 JP 00P 206860,31-JUL-2000 JP 00P 235274 PI
SACHIO SHIBATA,KENICHI HORIKOSHI,YOSHIO TANIYAMA,YASUSHI PI
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PC A61P43/00,G01N33/15,G01N33/50
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Query Match      100.0%; Score 1038; DB 6; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      721  CTCTATTCTCTCGACGGTGCCTCGAGTGCCTCGCATCCCTCTGTCCATCGGGGCCCTG 780
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Db      1021  CACATTGTTGAGTGGCAC 1038

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DEFINITION Sequence 23 from Patent WO0136471.
ACCESSION  AX148182
VERSION     AX148182.1  GI:14347084
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Chen, R., Dang, H.T. and Lowitz, K.P.
TITLE       Endogenous and non-endogenous versions of human g protein-coupled
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JOURNAL     Patent: WO 0136471-A 23 25-MAY-2001;
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Query Match      100.0%; Score 1038; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      361  CACCACGGGTGGAACACTATCTCCACGGGTGGGGCTGGGCAATGCTGCAACCTGTGG 420
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DEFINITION Sequence 1 from Patent WO0173029.
ACCESSION  AX299705
VERSION     AX299705.1  GI:17129250
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Ye, J.C., Cravchik, A.C., di Francesco, V.C. and Beasley, E.M.
TITLE       Isolated human g-protein coupled receptors, nucleic acid molecules
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JOURNAL     Patent: WO 0173029-A 1 04-OCT-2001;
            PE Corporation (NY) (US)
FEATURES    Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1021 CACATTGTGAGTGGCAC 1038

RESULT 6
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LOCUS
DEFINITION
ACCESSION AX375434
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Lannoy, V., Brezillon, S., Dethieux, M., Parmentier, M. and Govarts, C.
A recombinant cell line expressing gpcr11 as a functional receptor
validated by angiotensin and useful for screening of agonists and
antagonists
Patent: WO 0198330-A 11 27-DEC-2001;
Euroscreen S.A. (BE)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-254;
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QY 1 ATGTACAAACGGGTCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCCCGCG 60
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DEFINITION Sequence 79 from Patent W002064789.
ACCESSION AX521883
VERSION AX521883.1 GI:24410790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lind, P., Parodi, L. A., Vogeli, G. and Wood, L. S.
TITLE G protein-coupled receptor
JOURNAL Patent: WO 02064789-A 79 22-AUG-2002;
PHARMACIA & UPJOHN COMPANY [US]
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTGCTCATTTGTGGCCTTTGTGCTGGCGCACCTAGGCAATGGGCTCGCCCTGTGTGTTTC 120
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Best Local Similarity 100.0%; Pred. No. 1.3e-254; Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db 1021 CACATTTGTGATGGCAC 1038

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LOCUS Homo sapiens G protein-coupled receptor (GPR81) gene, complete cds.
ACCESSION AF411110
VERSION AF411110.1 GI:16566325
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1041)
Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458557
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2 (bases 1 to 1041)
Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Raddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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Query Match 100.0%; Score 1038; DB 9; Length 1041;
Best Local Similarity 100.0%; Pred. No. 1.3e-254; Indels 0; Gaps 0;
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QY 1 ATGTACACGGTCTGTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATCGCGCG 60
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LOCUS AX338371 1050 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 1 from Patent WO0174904.
ACCESSION AX338371
VERSION AX338371.1 GI:18128869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Majumder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Spaderina,S.K., Padigaru,M., Mishnu,V.S., Tchernev,V.T., Spytek,K.A., Li,L., Baumgartner,J.C. and Gusev,V.Y.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0174904-A 1 11-OCT-2001;
Curagen Corporation (US)
FEATURES
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ORIGIN
Query Match 100.0%; Score 1038; DB 6; Length 1050;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 1038; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTACAAAGGGTCTGCTGCGGATCGAGGGGACACCATCTCCAGGTGATGCGCGG 60
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RESULT 13
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LOCUS AX338373 1050 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3 from Patent WO0174904.
ACCESSION AX338373
VERSION AX338373.1 GI:18128870
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KEYWORDS      Homo sapiens (human)
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ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS      Majumder, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderma, S.K.,
Padigar, M., Mishra, V.S., Tchernev, V.T., Spytek, K.A., Li, L.,
Baumgartner, J.C. and Gusev, V.Y.
TITLE        Novel proteins and nucleic acids encoding same
JOURNAL      Patent: WO 0174904-A 3 11-OCT-2001;
Curagen Corporation (US)
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Query Match      100.0%; Score 1038; DB 6; Length 1050;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
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QY 1 ATGTACACGGGTCGTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCG 60
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LOCUS
DEFINITION   Sequence 11 from Patent WO0187937.
ACCESSION   AX305131
VERSION     AX305131.1 GI:17644766
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Patterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M.,
Graul, R., Khan, F.A., Gandhi, A.R., Walla, N.K., Nguyen, D.B., Yue, H.,
Hafalia, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A., Tang, T.Y.
and Au-Yang, J.
TITLE        G-protein coupled receptors
JOURNAL      Patent: WO 0187937-A 11 22-NOV-2001;
Incyte Genomics, Inc. (US)
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ACCESSION AX549382
VERSION AX549382.1 GI:25814001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 667 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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